

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 03:12:21 ; Search time 2619 Seconds
(without alignments)
10545.809 Million cell updates/sec

Title: US-09-989-731-407

Perfect score: 570
Sequence: 1 ggcgagcaggcggtacaaag.....aaaaaaaaaaaaaaaaaaaaa 570

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	570	100.0	570	6	AR252648	Sequence
2	570	100.0	570	6	AX403520	Sequence
3	570	100.0	570	9	AY359064	Homo sapi
4	569	99.8	569	6	AX201348	Sequence
5	529	92.8	543	6	BD222719	Human sig
6	529	92.8	543	6	BD226775	A novel m
7	519	91.1	519	6	BD082142	Reagents
8	518.6	91.0	562	6	BD082141	Reagents
9	513	90.0	530	9	BC072673	Homo sapi
10	503	88.2	503	9	BC029176	Homo sapi
11	471	82.6	471	9	HUMZ5210	Homo sapi
12	461	80.9	461	9	AF436839	Homo sapi
13	457.8	80.3	461	6	CQ76781	Sequence
14	457.8	80.3	461	6	AY040564	Homo sapi
15	345.4	60.6	347	9	AF313458	Homo sapi
16	293.4	51.5	380	6	AX334451	Sequence
17	291	51.1	291	6	CQ714558	Sequence
18	241.4	42.4	244	6	BD082138	Reagents
19	241.4	42.4	130129	2	AC108083	Homo sapi

20	241.4	42.4	166777	2	AC106813 Homo sapi
21	241.4	42.4	168347	2	AC025336 Homo sapi
22	241.4	42.4	190024	4	AC122714 Homo sapi
23	230.4	40.4	127488	2	AC022095 Homo sapi
24	225	39.5	225	6	BD082139 Reagents
25	144	25.3	190	6	BD082137 Reagents
26	135.2	23.7	525	10	AF313456 Mus muscu
27	118	20.7	630	10	AF313457 Mus muscu
28	115.8	20.3	377	10	AF36840 Mus muscu
29	114	20.0	114	6	BD082140 Reagents
30	110.6	19.4	331	10	AF36841 Ratlus no
31	93.6	16.4	245659	2	AC098957 Ratlus no
32	93.6	16.4	283593	2	AC131433 Ratlus no
33	91	16.0	254981	10	AL606479 Mouse DNA
34	75.6	13.3	130129	2	AC108083 Homo sapi
35	74.6	13.1	664	10	BC061046 Homo sapi
36	69.4	12.2	1613	6	E23142 Homo sapi
37	69	12.1	623	5	BC067658 Homo sapi
38	69	12.1	1898	6	I46765 Sequence 1
39	68.8	12.1	1507	9	BC002839 Homo sapi
40	68.8	12.1	1519	9	BC064621 Homo sapi
41	68.8	12.1	1798	9	BC042845 Homo sapi
42	68.6	12.0	1791	9	BC036709 Homo sapi
43	68	11.9	862	6	AX575614 Sequence
44	67.4	11.8	566	6	BD260638 49 human
45	67.4	11.8	1451	9	BC002816 Homo sapi
46	67.4	11.8	2070	9	BC074500 Homo sapi
47	67.4	11.8	3819	5	BC076831 Homo sapi
48	67	11.8	733	6	CQ769552 Sequence
49	67	11.8	733	6	CQ769554 Sequence
50	67	11.8	820	9	BC000785 Homo sapi
51	67	11.8	880	9	AF207829 Homo sapi
52	66.6	11.7	9884	6	AX347361 Sequence
53	66.6	11.7	9884	6	AX349082 Sequence
54	66.6	11.7	9884	6	AX657761 Sequence
55	66.6	11.7	9884	6	AX659035 Sequence
56	66.4	11.6	678	9	BC003602 Homo sapi
57	66.4	11.6	3985	5	RNGPROCR Homo sapi
58	66.2	11.6	1398	5	BC084466 Homo sapi
59	66.2	11.6	1774	10	BC028989 Homo sapi
60	66.2	11.6	2799	10	BC054462 Homo sapi
61	66.2	11.6	4143	5	GSDYNACT Homo sapi
62	66	11.5	974	9	BC056410 Homo sapi
63	65.6	11.5	550	6	CQ821498 Sequence
64	65.6	11.5	550	9	BC024232 Homo sapi
65	65.6	11.5	562	9	BC053376 Homo sapi
66	65.6	11.5	923	10	BC049576 Homo sapi
67	65.6	11.5	2805	9	BC025665 Homo sapi
68	65.6	11.5	2965	10	BC057094 Homo sapi
69	65.4	11.5	527	9	BC032225 Homo sapi
70	65.4	11.5	646	6	BD266891 Homo sapi
71	65.4	11.5	1723	6	AX816464 Sequence
72	65.4	11.5	1723	9	BC012944 Homo sapi
73	65.4	11.5	2532	5	BC055227 Danio rer
74	65.4	11.5	3462	9	BC032668 Homo sapi
75	65.2	11.4	141	6	AR425949 Sequence
76	65.2	11.4	141	6	AX986643 Sequence
77	65.2	11.4	141	6	BD121502 EST and e
78	65.2	11.4	681	5	BC055187 Homo sapi
79	65.2	11.4	1693	9	BC064214 Xenopus t
80	65.2	11.4	2146	9	BC039148 Homo sapi
81	65	11.4	140	6	AR425952 Sequence
82	65	11.4	140	6	AX986646 Sequence
83	65	11.4	140	6	BD121505 EST and e
84	65	11.4	148	6	AR425950 Sequence
85	65	11.4	148	6	AR425953 Sequence
86	65	11.4	148	6	AX986644 Sequence
87	65	11.4	148	6	AX986647 Sequence
88	65	11.4	148	6	BD121503 EST and e
89	65	11.4	148	6	BD121506 EST and e
90	65	11.4	153	6	AR425954 Sequence
91	65	11.4	153	6	AX986648 Sequence
92	65	11.4	153	6	BD121507 EST and e

93	65	11.4	861	9	AK026600	AK026600 Homo sapi	166	63	11.1	394	6	C0525359	C0525359 Sequence
94	65	11.4	1986	9	BC002948	BC002948 Homo sapi	167	63	11.1	407	5	BC073638	BC073638 Xenopus 1
95	65	11.4	2090	2	BC037555	BC037555 Homo sapi	168	63	11.1	407	5	C0525256	C0525256 Sequence
96	65	11.4	17553	2	AP001096	AP001096 Homo sapi	169	63	11.1	562	10	BC049688	BC049688 Mus muscu
97	64.8	11.4	326	6	C0527450	C0527450 Sequence	170	63	11.1	893	5	BC077861	BC077861 Xenopus 1
98	64.8	11.4	983	6	BC005007	BC005007 Homo sapi	171	63	11.1	1129	9	BC013587	BC013587 Homo sapi
99	64.8	11.4	1023	5	BC011708	BC011708 Homo sapi	172	63	11.1	1490	9	BC001236	BC001236 Homo sapi
100	64.8	11.4	1026	5	BC084480	BC084480 Xenopus t	173	63	11.1	1539	9	BC002372	BC002372 Homo sapi
101	64.8	11.4	1050	6	BD218576	BD218576 71 human	174	63	11.1	2299	3	AK16078	AK16078 Homo sapi
102	64.8	11.4	1390	6	BD260732	BD260732 50 human	175	63	11.1	2239	3	AK025573	AK025573 Homo sapi
103	64.8	11.4	3327	10	BC028272	BC028272 Mus muscu	176	63	11.1	2335	6	AX834748	AX834748 Sequence
104	64.8	11.4	3329	10	BC054371	BC054371 Mus muscu	177	63	11.1	2335	6	AX834748	AX834748 Sequence
105	64.6	11.3	159	6	AR425951	AR425951 Sequence	178	63	11.1	2385	5	BC072951	BC072951 Homo sapi
106	64.6	11.3	159	6	AX986645	AX986645 Sequence	179	63	11.1	2385	5	BC072951	BC072951 Homo sapi
107	64.6	11.3	159	6	BD121504	BD121504 EST and e	180	63	11.1	113541	2	AC023769	AC023769 Homo sapi
108	64.6	11.3	503	6	AX548518	AX548518 Sequence	181	62.8	11.0	315	6	AR423832	AR423832 Sequence
109	64.6	11.3	1718	10	AF411056	AF411056 Rattus no	182	62.8	11.0	315	6	AX984526	AX984526 Sequence
110	64.6	11.3	1868	10	BC032280	BC032280 Mus muscu	183	62.8	11.0	841	5	BC059599	BC059599 Danio rer
111	64.4	11.3	1277	5	BC074288	BC074288 Xenopus 1	184	62.8	11.0	1198	9	BC004529	BC004529 Mus muscu
112	64.4	11.3	2037	4	AF200416	AF200416 Equus cab	185	62.8	11.0	1198	9	BC004529	BC004529 Mus muscu
113	64.4	11.3	1717	4	BC001963	BC001963 Homo sapi	186	62.8	11.0	1586	10	BC000051	BC000051 Homo sapi
114	64.4	11.3	2526	5	BC007392	BC007392 Xenopus 1	187	62.8	11.0	1730	9	BC048345	BC048345 Homo sapi
115	64.4	11.3	162345	2	AC147606	AC147606 Mus muscu	188	62.8	11.0	1843	9	BC038796	BC038796 Homo sapi
116	64.2	11.3	144	6	AX986649	AX986649 Sequence	189	62.8	11.0	1894	10	BC039124	BC039124 Mus muscu
117	64.2	11.3	144	6	BD121508	BD121508 EST and e	190	62.8	11.0	2042	6	AX086394	AX086394 Sequence
118	64.2	11.3	495	6	C0433520	C0433520 Sequence	191	62.8	11.0	2139	2	AC146916	AC146916 Rattus no
119	64.2	11.3	1592	9	BC015787	BC015787 Homo sapi	192	62.8	11.0	2139	2	AC146916	AC146916 Rattus no
120	64.2	11.3	2116	9	BC063648	BC063648 Mus muscu	193	62.6	11.0	201	6	C0526416	C0526416 Sequence
121	64.2	11.3	19398	2	AC102269	AC102269 Mus muscu	194	62.6	11.0	337	6	C0529025	C0529025 Sequence
122	64.2	11.3	2116	9	AF028823	AF028823 Homo sapi	195	62.6	11.0	511	5	BC078541	BC078541 Xenopus 1
123	64	11.2	1451	9	BC010430	BC010430 Homo sapi	196	62.6	11.0	587	6	BD275408	BD275408 Homo sapi
124	64	11.2	1554	9	BC061634	BC061634 Mus muscu	197	62.6	11.0	1442	9	HSM607864	HSM607864 Sequence
125	64	11.2	1559	10	BC070084	BC070084 Homo sapi	198	62.6	11.0	1760	10	BC027078	BC027078 Homo sapi
126	64	11.2	1590	10	BC072486	BC072486 Rattus no	199	62.6	11.0	2302	9	BC002356	BC002356 Homo sapi
127	64	11.2	1888	9	BC037108	BC037108 Homo sapi	200	62.6	11.0	2311	6	AX779817	AX779817 Sequence
128	64	11.2	1888	9	BC033677	BC033677 Homo sapi	201	62.6	11.0	2311	6	AX779817	AX779817 Sequence
129	64	11.2	2158	9	AB044547	AB044547 Homo sapi	202	62.6	11.0	2311	6	AX779817	AX779817 Sequence
130	64	11.2	2158	9	BC051021	BC051021 Mus muscu	203	62.6	11.0	2432	5	BC082653	BC082653 Xenopus 1
131	64	11.2	2490	10	BC083550	BC083550 Rattus no	204	62.6	11.0	2589	6	AR129832	AR129832 Sequence
132	64	11.2	2674	10	BC083550	BC083550 Rattus no	205	62.6	11.0	2732	6	AX196286	AX196286 Sequence
133	63.8	11.2	734	6	BD107842	BD107842 Homo sapi	206	62.6	11.0	2732	6	AX358826	AX358826 Sequence
134	63.8	11.2	1621	6	BD107842	BD107842 Homo sapi	207	62.6	11.0	2732	6	AX358826	AX358826 Sequence
135	63.8	11.2	2936	5	HSM801417	HSM801417 Homo sapi	208	62.6	11.0	2732	6	AX358826	AX358826 Sequence
136	63.8	11.2	2951	5	HSM801417	HSM801417 Homo sapi	209	62.6	11.0	2732	6	AX358826	AX358826 Sequence
137	63.8	11.2	214442	10	AC126115	AC126115 Rattus no	210	62.6	11.0	2732	6	AX358826	AX358826 Sequence
138	63.6	11.2	449	6	C0423617	C0423617 Sequence	211	62.6	11.0	2732	6	AX358826	AX358826 Sequence
139	63.6	11.2	481	6	BC070219	BC070219 Homo sapi	212	62.6	11.0	3049	9	AX359089	AX359089 Homo sapi
140	63.6	11.2	1087	3	BC043795	BC043795 Homo sapi	213	62.6	11.0	3049	9	AX359089	AX359089 Homo sapi
141	63.6	11.2	1090	3	AY069454	AY069454 Drosophila	214	62.6	11.0	3049	9	AX359089	AX359089 Homo sapi
142	63.6	11.2	1307	6	AR083266	AR083266 Sequence	215	62.4	10.9	33476	2	AC098488	AC098488 Sequence
143	63.6	11.2	1307	6	BD092208	BD092208 Secreted	216	62.4	10.9	337	6	C0527057	C0527057 Sequence
144	63.6	11.2	2465	5	BC070798	BC070798 Xenopus 1	217	62.4	10.9	422	6	C0433395	C0433395 Sequence
145	63.6	11.2	4750	5	BC066499	BC066499 Danio rer	218	62.4	10.9	422	6	C0433395	C0433395 Sequence
146	63.4	11.1	451	6	BD219559	BD219559 Human gen	219	62.4	10.9	422	6	C0433395	C0433395 Sequence
147	63.4	11.1	1280	9	BC034690	BC034690 Homo sapi	220	62.4	10.9	422	6	C0433395	C0433395 Sequence
148	63.4	11.1	1280	9	BC034690	BC034690 Homo sapi	221	62.4	10.9	422	6	C0433395	C0433395 Sequence
149	63.4	11.1	1550	9	BC047312	BC047312 Homo sapi	222	62.4	10.9	422	6	C0433395	C0433395 Sequence
150	63.4	11.1	1554	9	BC033613	BC033613 Mus muscu	223	62.4	10.9	422	6	C0433395	C0433395 Sequence
151	63.4	11.1	1554	9	BC033613	BC033613 Mus muscu	224	62.4	10.9	422	6	C0433395	C0433395 Sequence
152	63.4	11.1	2576	10	BC040761	BC040761 Mus muscu	225	62.4	10.9	422	6	C0433395	C0433395 Sequence
153	63.4	11.1	2576	10	BC040761	BC040761 Mus muscu	226	62.4	10.9	422	6	C0433395	C0433395 Sequence
154	63.4	11.1	3336	5	BC054630	BC054630 Danio rer	227	62.4	10.9	422	6	C0433395	C0433395 Sequence
155	63.4	11.1	6582	5	AX481755	AX481755 Sequence	228	62.4	10.9	422	6	C0433395	C0433395 Sequence
156	63.2	11.1	446	9	BC065233	BC065233 Sequence	229	62.4	10.9	422	6	C0433395	C0433395 Sequence
157	63.2	11.1	474	6	C0523622	C0523622 Sequence	230	62.4	10.9	422	6	C0433395	C0433395 Sequence
158	63.2	11.1	598	6	CQ426520	CQ426520 Sequence	231	62.4	10.9	422	6	C0433395	C0433395 Sequence
159	63.2	11.1	882	5	AK025483	AK025483 Homo sapi	232	62.4	10.9	422	6	C0433395	C0433395 Sequence
160	63.2	11.1	1252	5	BC054251	BC054251 Homo sapi	233	62.4	10.9	422	6	C0433395	C0433395 Sequence
161	63.2	11.1	1990	5	AK098817	AK098817 Homo sapi	234	62.4	10.9	422	6	C0433395	C0433395 Sequence
162	63.2	11.1	2230	5	BC067188	BC067188 Danio rer	235	62.4	10.9	422	6	C0433395	C0433395 Sequence
163	63.2	11.1	6262	9	HSM807046	HSM807046 Homo sapi	236	62.4	10.9	422	6	C0433395	C0433395 Sequence
164	63.2	11.1	161823	2	AC136947	AC136947 Homo sapi	237	62.4	10.9	422	6	C0433395	C0433395 Sequence
165	63.2	11.1	218821	2	AC116238	AC116238 Rattus no	238	62.4	10.9	422	6	C0433395	C0433395 Sequence
			2	AC097592	AC097592 Rattus no								

C 239	62.2	10.9	448	6	CQ411846	CQ411846 Sequence	312	61.8	10.8	1484	9	AY358586	AY358586 Homo sapi
C 240	62.2	10.9	550	6	CQ524549	CQ524549 Sequence	313	61.8	10.8	1739	9	AB060873	AB060873 Macaca fa
241	62.2	10.9	623	10	BC059150	BC059150 Rattus no	314	61.8	10.8	1740	9	BC072395	BC072395 Homo sapi
242	62.2	10.9	947	5	AF266204	AF266204 Gallinich	315	61.8	10.8	2076	10	BC010309	BC010309 Mus muscu
243	62.2	10.9	1100	5	BC082894	BC082894 Xenopus t	316	61.8	10.8	2082	6	AR059958	AR059958 Sequence
244	62.2	10.9	1422	5	BC080890	BC080890 Xenopus t	317	61.8	10.8	2093	8	AB089677	AB089677 Prunus pe
245	62.2	10.9	1537	9	BSM803079	ALU713709 Homo sapi	318	61.8	10.8	2158	10	BC031195	BC031195 Mus muscu
246	62.2	10.9	1584	5	BC042270	BC042270 Xenopus t	319	61.8	10.8	2195	9	BC009484	BC009484 Homo sapi
247	62.2	10.9	1679	9	BC018747	BC018747 Homo sapi	320	61.8	10.8	2291	9	BSM803423	BSM803423 Homo sapi
248	62.2	10.9	1680	10	BC049920	BC049920 Mus muscu	321	61.8	10.8	2249	9	BC073963	BC073963 Homo sapi
249	62.2	10.9	1848	9	BC053543	BC053543 Homo sapi	322	61.8	10.8	2376	9	BC016664	BC016664 Homo sapi
250	62.2	10.9	1950	9	BC033818	BC033818 Homo sapi	323	61.8	10.8	3225	5	BC063722	BC063722 Mus muscu
251	62.2	10.9	1986	5	BC074553	BC074553 Xenopus t	324	61.8	10.8	3665	10	BC046598	BC046598 Homo sapi
252	62.2	10.9	1996	6	BC011143	BC011143 Homo sapi	325	61.8	10.8	3737	9	BC024592	BC024592 Homo sapi
253	62.2	10.9	2329	6	AR374711	AR374711 Sequence	326	61.8	10.8	3985	9	BC063876	BC063876 Homo sapi
254	62.2	10.9	2403	9	BC063892	BC063892 Homo sapi	C 327	61.8	10.8	184332	2	AC141745	AC141745 Apis mell
255	62.2	10.9	2448	9	BC053867	BC053867 Homo sapi	328	61.6	10.8	442	6	CQ524766	CQ524766 Sequence
256	62.2	10.9	2846	6	AR170129	AR170129 Sequence	329	61.6	10.8	458	6	CQ516306	CQ516306 Sequence
C 257	62.2	10.9	2836	6	AR170130	AR170130 Sequence	330	61.6	10.8	541	6	CQ522930	CQ522930 Sequence
258	62.2	10.9	2836	6	AR438727	AR438727 Sequence	331	61.6	10.8	887	9	AB125184	AB125184 Macaca fa
C 259	62.2	10.9	2836	6	AR438728	AR438728 Sequence	332	61.6	10.8	1237	9	BC058927	BC058927 Homo sapi
C 260	62.2	10.9	2836	6	BD069549	BD069549 Novel car	333	61.6	10.8	1301	10	BC016453	BC016453 Mus muscu
C 261	62.2	10.9	2836	6	BD069550	BD069550 Novel car	334	61.6	10.8	1331	10	BC048735	BC048735 Homo sapi
C 262	62.2	10.9	3018	12	AY452085	AY452085 Cloning v	335	61.6	10.8	1591	10	AF087943	AF087943 Homo sapi
263	62.2	10.9	3141	9	BSM805106	AL833829 Homo sapi	336	61.6	10.8	1591	10	BC062406	BC062406 Xenopus no
264	62.2	10.9	3309	10	BC051423	BC051423 Mus muscu	337	61.6	10.8	1607	10	BC048697	BC048697 Mus muscu
265	62.2	10.9	3338	10	BSM803596	AL832388 Homo sapi	338	61.6	10.8	1630	5	BC055215	BC055215 Danio rer
266	62.2	10.9	3836	9	BC063854	BC063854 Homo sapi	339	61.6	10.8	1594	9	BSM806665	BSM806665 Homo sapi
267	62.2	10.9	6085	10	BC053387	BC053387 Mus muscu	340	61.6	10.8	1769	9	BC025749	BC025749 Homo sapi
C 268	62.2	10.9	6256	6	AX346318	AX346318 Sequence	341	61.6	10.8	1770	10	BC062406	BC062406 Rattus no
269	62.2	10.9	203822	2	AC073698	AC073698 Mus muscu	342	61.6	10.8	1849	5	BC080995	BC080995 Homo sapi
270	62.2	10.9	256673	2	AC087716	AC087716 Mus muscu	343	61.6	10.8	1925	5	BC066381	BC066381 Danio rer
271	62	10.9	166	6	CQ708897	CQ708897 Sequence	344	61.6	10.8	2117	9	BC024300	BC024300 Homo sapi
272	62	10.9	190	6	AR425287	AR425287 Sequence	345	61.6	10.8	2127	9	BC024300	BC024300 Homo sapi
273	62	10.9	190	6	AX985981	AX985981 Sequence	346	61.6	10.8	2368	9	BSM802593	BSM802593 Homo sapi
274	62	10.9	190	6	BD120840	BD120840 EST and e	347	61.6	10.8	2376	3	AK112359	AK112359 Clona int
275	62	10.9	216	6	CQ525990	CQ525990 Sequence	C 348	61.6	10.8	2795	8	CBKPMERGN	CBKPMERGN Homo sapi
276	62	10.9	246	6	AR422120	AR422120 Sequence	349	61.6	10.8	2843	6	CQ488472	CQ488472 Sequence
277	62	10.9	246	6	AX982814	AX982814 Sequence	350	61.6	10.8	2843	6	CQ488693	CQ488693 Sequence
278	62	10.9	246	6	BD117673	BD117673 EST and e	351	61.6	10.8	2843	6	CQ491011	CQ491011 Sequence
C 279	62	10.9	360	6	CQ529133	CQ529133 Sequence	352	61.6	10.8	2843	6	CQ491990	CQ491990 Sequence
280	62	10.9	534	9	BC011021	BC011021 Homo sapi	353	61.6	10.8	2843	6	CQ492097	CQ492097 Sequence
281	62	10.9	722	9	BC042671	BC042671 Homo sapi	354	61.6	10.8	2843	6	CQ492259	CQ492259 Sequence
282	62	10.9	854	5	BC080013	BC080013 Xenopus t	355	61.6	10.8	2843	6	CQ494303	CQ494303 Sequence
283	62	10.9	964	9	BC009341	BC009341 Homo sapi	356	61.6	10.8	2843	6	CQ494530	CQ494530 Sequence
284	62	10.9	985	6	BD134733	BD134733 31 Human	357	61.6	10.8	2843	6	CQ496867	CQ496867 Sequence
285	62	10.9	1603	9	BC015756	BC015756 Homo sapi	358	61.6	10.8	2843	6	CQ497898	CQ497898 Sequence
286	62	10.9	1627	9	BC002519	BC002519 Homo sapi	359	61.6	10.8	2843	6	CQ498011	CQ498011 Sequence
287	62	10.9	1816	5	BC055610	BC055610 Danio rer	360	61.6	10.8	3050	5	AB125660	AB125660 Gallus ga
288	62	10.9	1935	9	BSM802519	AL119953 Homo sapi	361	61.6	10.8	3092	9	BC050377	BC050377 Homo sapi
289	62	10.9	2138	10	BC035945	BC035945 Mus muscu	362	61.6	10.8	3607	5	BC075569	BC075569 Xenopus t
290	62	10.9	2175	5	AB056480	AB056480 Rana cate	363	61.6	10.8	3683	9	BSM808647	BSM808647 Homo sapi
291	62	10.9	2847	10	BC027028	BC027028 Mus muscu	364	61.6	10.8	4168	6	AX393305	AX393305 Sequence
292	62	10.9	3154	10	BC006874	BC006874 Mus muscu	365	61.6	10.8	5277	9	BSM807015	BSM807015 Homo sapi
293	62	10.9	3459	6	AX348086	AX348086 Sequence	366	61.6	10.8	126290	2	AC099483	AC099483 Sequence
294	62	10.9	3459	6	AX348086	AX348086 Sequence	367	61.6	10.8	239	6	CQ524654	CQ524654 Sequence
295	62	10.9	152252	2	AC147683	AC147683 Pan trogl	368	61.4	10.8	257	6	AX334682	AX334682 Sequence
296	62	10.9	333321	3	AC116986	AC116986 Dictyoste	369	61.4	10.8	257	6	AX410615	AX410615 Sequence
297	61.8	10.8	447	10	BC055352	BC055352 Mus muscu	370	61.4	10.8	383	5	BC076322	BC076322 Danio rer
298	61.8	10.8	527	9	AK026542	AK026542 Homo sapi	371	61.4	10.8	457	10	BC064074	BC064074 Mus muscu
299	61.8	10.8	539	6	CQ655454	CQ655454 Sequence	372	61.4	10.8	505	6	CQ524936	CQ524936 Sequence
300	61.8	10.8	599	6	CQ627650	CQ627650 Sequence	373	61.4	10.8	571	8	AY554050	AY554050 Oryza sat
301	61.8	10.8	739	6	CQ769575	CQ769575 Sequence	374	61.4	10.8	762	3	LN512840	LN512840 Lethoceru
302	61.8	10.8	739	6	CQ769591	CQ769591 Sequence	375	61.4	10.8	775	9	BC056238	BC056238 Homo sapi
303	61.8	10.8	739	6	CQ769608	CQ769608 Sequence	C 376	61.4	10.8	794	6	BD018939	BD018939 Novel gen
C 304	61.8	10.8	754	6	BD018741	BD018741 Novel gen	C 377	61.4	10.8	794	6	BD098877	BD098877 Novel gen
C 305	61.8	10.8	754	6	BD098679	BD098679 Novel gen	378	61.4	10.8	1181	10	BC049768	BC049768 Mus muscu
C 306	61.8	10.8	835	10	AF260436	AF260436 Rattus no	379	61.4	10.8	1234	10	BC007381	BC007381 Homo sapi
307	61.8	10.8	1261	9	BC073957	BC073957 Homo sapi	380	61.4	10.8	1245	5	BC058310	BC058310 Homo sapi
308	61.8	10.8	1476	6	BD227281	BD227281 Secreted	381	61.4	10.8	1316	9	BSM801735	BSM801735 Homo sapi
309	61.8	10.8	1484	6	AR252570	AR252570 Sequence	382	61.4	10.8	1554	5	AF065135	AF065135 Xenopus t
310	61.8	10.8	1484	6	AX376152	AX376152 Sequence	383	61.4	10.8	1554	6	BD132843	BD132843 W545 com
311	61.8	10.8	1484	6	AX403405	AX403405 Sequence	384	61.4	10.8	1554	6	CQ776558	CQ776558 Sequence

531	60.8	10.7	1779	6	AX251708	Sequence	604	60.6	10.6	2820	6	CQ776753	CQ776753 Sequence
532	60.8	10.7	1882	10	BC017147	Mus muscu	605	60.6	10.6	2820	9	BC025256	BC025256 Homo sapi
533	60.8	10.7	2084	10	BC058744	Mus muscu	606	60.6	10.6	2968	10	BC058408	BC058408 Homo sapi
534	60.8	10.7	2084	10	BC062164	Mus muscu	607	60.6	10.6	3099	10	BC055299	BC055299 Mus muscu
535	60.8	10.7	2116	9	BC031644	Mus muscu	608	60.6	10.6	3581	9	BC038669	BC038669 Homo sapi
536	60.8	10.7	2116	6	AX364833	Sequence	609	60.6	10.6	3724	9	BSM804529	BSM804529 Homo sapi
537	60.8	10.7	2173	9	BC063384	Mus muscu	610	60.6	10.6	5135	10	BC061470	BC061470 Mus muscu
538	60.8	10.7	2533	5	BC064702	Danio rer	611	60.6	10.6	6250	9	BSM807742	BSM807742 Homo sapi
539	60.8	10.7	2600	10	BC037001	Mus muscu	612	60.6	10.6	6559	5	BC063724	BC063724 Xenopus 1
540	60.8	10.7	2628	9	BC034992	Mus muscu	613	60.4	10.6	306	6	CQ423767	CQ423767 Sequence
541	60.8	10.7	3180	10	S79832	transcript	614	60.4	10.6	397	6	CQ517563	CQ517563 Sequence
542	60.8	10.7	3508	6	BD227241	Secreted	615	60.4	10.6	407	6	CQ528868	CQ528868 Sequence
543	60.8	10.7	4128	10	AF022363	Mus muscu	616	60.4	10.6	449	6	CQ526770	CQ526770 Sequence
544	60.8	10.7	4259	9	BSM805206	AF324064 Homo sapi	617	60.4	10.6	657	10	BC035943	BC035943 Mus muscu
545	60.8	10.7	6200	9	AF324064	Mus muscu	618	60.4	10.6	731	6	CQ431866	CQ431866 Sequence
546	60.8	10.7	70705	2	AC101621	Mus muscu	619	60.4	10.6	722	6	CQ431102	CQ431102 Sequence
547	60.8	10.7	153567	2	AC087145	Mus muscu	620	60.4	10.6	792	10	BC006585	BC006585 Mus muscu
548	60.8	10.7	171260	2	CR812474	Danio rer	621	60.4	10.6	944	9	BC018640	BC018640 Homo sapi
549	60.8	10.7	218010	2	AC116052	AC116052 Mus muscu	622	60.4	10.6	1048	3	AY069195	AY069195 Drosophila
550	60.8	10.7	223920	2	AC141733	Apis mell	623	60.4	10.6	1051	9	BC070489	BC070489 Homo sapi
551	60.6	10.6	188	6	AR418867	Sequence	624	60.4	10.6	1115	10	BC049678	BC049678 Mus muscu
552	60.6	10.6	188	6	AX979561	Sequence	625	60.4	10.6	1358	9	AF022813	AF022813 Homo sapi
553	60.6	10.6	188	6	BD114420	EST and e	626	60.4	10.6	1454	5	BC064706	BC064706 Danio rer
554	60.6	10.6	201	11	BY202595	Sequence	627	60.4	10.6	1524	5	BC067624	BC067624 Danio rer
555	60.6	10.6	267	6	CQ526755	Sequence	628	60.4	10.6	1561	9	AF217966	AF217966 Homo sapi
556	60.6	10.6	447	9	AK026855	Mus muscu	629	60.4	10.6	1595	9	BC035626	BC035626 Homo sapi
557	60.6	10.6	458	10	BC061002	Mus muscu	630	60.4	10.6	1627	10	BC043926	BC043926 Mus muscu
558	60.6	10.6	640	3	BT001518	Drosophila	631	60.4	10.6	1630	9	BC029864	BC029864 Homo sapi
559	60.6	10.6	700	9	BC035864	BC035864 Homo sapi	632	60.4	10.6	1638	10	BC030439	BC030439 Mus muscu
560	60.6	10.6	766	6	108319	Sequence 1	633	60.4	10.6	1702	10	BC057136	BC057136 Homo sapi
561	60.6	10.6	789	9	BC017112	BC017112 Homo sapi	634	60.4	10.6	1710	9	BC064395	BC064395 Mus muscu
562	60.6	10.6	805	10	BC063183	Rattus no	635	60.4	10.6	1731	9	BC001554	BC001554 Homo sapi
563	60.6	10.6	860	6	BD260192	50 human	636	60.4	10.6	1851	10	BC017684	BC017684 Mus muscu
564	60.6	10.6	1076	9	BC050446	Homo sapi	637	60.4	10.6	1879	10	BC060146	BC060146 Mus muscu
565	60.6	10.6	1091	6	AR271010	Sequence	638	60.4	10.6	1919	10	BC057964	BC057964 Mus muscu
566	60.6	10.6	1091	6	AX053122	Sequence	639	60.4	10.6	1919	10	BC057964	BC057964 Mus muscu
567	60.6	10.6	1155	5	BC074027	Danio rer	640	60.4	10.6	1966	9	BSM808069	BSM808069 Homo sapi
568	60.6	10.6	1157	6	BD233739	31 human	641	60.4	10.6	2113	10	BC012405	BC012405 Homo sapi
569	60.6	10.6	1175	9	BC049386	Homo sapi	642	60.4	10.6	2156	3	AK116789	AK116789 Mus muscu
570	60.6	10.6	1194	9	BC016139	Homo sapi	643	60.4	10.6	2351	9	AB063077	AB063077 Macaca fa
571	60.6	10.6	1234	6	AX092332	Sequence	644	60.4	10.6	2701	9	BSM807920	BSM807920 Homo sapi
572	60.6	10.6	1234	6	AX376170	Sequence	645	60.4	10.6	2722	9	BSM806004	BSM806004 Homo sapi
573	60.6	10.6	1234	9	AY358438	Homo sapi	646	60.4	10.6	2739	10	BC055303	BC055303 Mus muscu
574	60.6	10.6	1339	9	BC048255	Homo sapi	647	60.4	10.6	2990	10	AF185576	AF185576 Mus muscu
575	60.6	10.6	1445	5	BC020080	Mus muscu	648	60.4	10.6	3204	10	BC075680	BC075680 Mus muscu
576	60.6	10.6	1480	5	BC066516	Danio rer	649	60.4	10.6	3264	9	BSM805112	BSM805112 Homo sapi
577	60.6	10.6	1505	5	BC067601	Danio rer	650	60.4	10.6	3327	10	BC028908	BC028908 Mus muscu
578	60.6	10.6	1638	10	BC057896	Mus muscu	651	60.4	10.6	3520	9	BC037406	BC037406 Homo sapi
579	60.6	10.6	1643	10	BC008512	Mus muscu	652	60.4	10.6	4077	5	BC075104	BC075104 Xenopus t
580	60.6	10.6	1684	9	BC034406	BC034406 Homo sapi	653	60.4	10.6	4452	9	BC051768	BC051768 Homo sapi
581	60.6	10.6	1788	5	BC084147	Xenopus t	654	60.4	10.6	4657	10	BC030187	BC030187 Mus muscu
582	60.6	10.6	1807	10	BC081928	Rattus no	655	60.4	10.6	5076	9	AB062750	AB062750 Homo sapi
583	60.6	10.6	1842	10	BC025589	Mus muscu	656	60.4	10.6	5630	9	BSM806073	BSM806073 Homo sapi
584	60.6	10.6	1866	9	BSM800618	BSM800618 Homo sapi	657	60.4	10.6	6702	9	AF378756	AF378756 Homo sapi
585	60.6	10.6	1904	9	BSM807438	BSM807438 Homo sapi	658	60.4	10.6	130701	2	AC009889	AC009889 Homo sapi
586	60.6	10.6	1953	9	BC029049	Homo sapi	659	60.4	10.6	160237	2	AC149093	AC149093 Pan trogl
587	60.6	10.6	1983	9	BC019338	Homo sapi	660	60.4	10.6	175059	2	AC140895	AC140895 Homo sapi
588	60.6	10.6	2000	6	BD252089	47 seetret	661	60.4	10.6	175785	2	AC016773	AC016773 Homo sapi
589	60.6	10.6	2040	5	BC066408	Danio rer	662	60.4	10.6	189223	3	AC016773	AC016773 Homo sapi
590	60.6	10.6	2060	6	AR310262	AR310262 Sequence	663	60.4	10.6	202705	2	AC149065	AC149065 Mus muscu
591	60.6	10.6	2070	10	BC052830	Mus muscu	664	60.4	10.6	211419	2	AC126760	AC126760 Homo sapi
592	60.6	10.6	2207	9	BC058880	Homo sapi	665	60.4	10.6	235330	2	AC140522	AC140522 Homo sapi
593	60.6	10.6	2229	9	BC015555	Homo sapi	666	60.4	10.6	291000	1	SC0939105	SC0939105 Streptomy
594	60.6	10.6	2307	9	BC032410	Homo sapi	667	60.4	10.6	349980	6	AX344554	AX344554 Sequence
595	60.6	10.6	2320	9	BC033810	Homo sapi	668	60.4	10.6	349980	6	AX344555	AX344555 Sequence
596	60.6	10.6	2403	9	BSM808752	BSM808752 Homo sapi	669	60.2	10.6	153	6	CQ700107	CQ700107 Sequence
597	60.6	10.6	2429	9	BC001056	Homo sapi	670	60.2	10.6	176	6	AR422406	AR422406 Sequence
598	60.6	10.6	2439	9	BC001823	Homo sapi	671	60.2	10.6	176	6	AX983100	AX983100 Sequence
599	60.6	10.6	2438	10	BC075617	Mus muscu	672	60.2	10.6	176	6	BD117959	BD117959 EST and e
600	60.6	10.6	2480	5	BC072229	Xenopus 1	673	60.2	10.6	231	6	CQ526354	CQ526354 Sequence
601	60.6	10.6	2485	10	BC064470	Mus muscu	674	60.2	10.6	261	6	CQ524617	CQ524617 Sequence
602	60.6	10.6	2514	9	BC044863	Homo sapi	675	60.2	10.6	291	6	CQ488160	CQ488160 Sequence
603	60.6	10.6	2792	10	AF177401	Spermophi	676	60.2	10.6	413	6	CQ517947	CQ517947 Sequence

677	60.2	10.6	471	6	COS22475	COS22475 Sequence	750	60.2	10.6	3308	9	BC035009	BC035009 Homo sapi
678	60.2	10.6	507	6	COS21478	COS21478 Sequence	751	60.2	10.6	3309	5	BC068420	BC068420 Danto rer
679	60.2	10.6	514	10	BC061178	BC061178 Mus muscu	752	60.2	10.6	3456	5	BC056871	BC056871 Homo sapi
680	60.2	10.6	515	6	COS26571	COS26571 Sequence	753	60.2	10.6	3492	5	BC078645	BC078645 Danto rer
681	60.2	10.6	527	6	COS27201	COS27201 Sequence	754	60.2	10.6	3830	5	BC071560	BC071560 Homo sapi
682	60.2	10.6	541	9	BC021886	BC021886 Homo sapi	755	60.2	10.6	4028	3	AF003106	AF003106 Homo sapi
683	60.2	10.6	542	9	BC040713	BC040713 Homo sapi	756	60.2	10.6	4135	9	HSM801979	HSM801979 Homo sapi
684	60.2	10.6	556	6	COS23722	COS23722 Sequence	757	60.2	10.6	4660	6	AX211375	AX211375 Homo sapi
685	60.2	10.6	713	10	BC002008	BC002008 Mus muscu	758	60.2	10.6	4697	4	BTTR0M2	BTTR0M2 Homo sapi
686	60.2	10.6	806	9	BC071709	BC071709 Homo sapi	759	60.2	10.6	5137	10	BC066082	BC066082 Homo sapi
687	60.2	10.6	869	3	BT011554	BT011554 Drosophi1	760	60.2	10.6	5534	6	AX780181	AX780181 Sequence
688	60.2	10.6	903	3	AY118755	AY118755 Drosophi1	761	60.2	10.6	5536	10	BC060705	BC060705 Mus muscu
689	60.2	10.6	910	10	BC069266	BC069266 Mus muscu	762	60.2	10.6	5539	10	BC049182	BC049182 Mus muscu
690	60.2	10.6	1000	10	BC064816	BC064816 Mus muscu	763	60.2	10.6	163018	10	AC132254	AC132254 Mus muscu
691	60.2	10.6	1029	3	AK174142	AK174142 Homo sapi	764	60.2	10.6	189728	10	AC140223	AC140223 Mus muscu
692	60.2	10.6	1087	9	BC015905	BC015905 Homo sapi	765	60.2	10.6	267093	2	AC109408	AC109408 Homo sapi
693	60.2	10.6	1092	10	BC005748	BC005748 Mus muscu	766	60.2	10.6	292100	1	SC093121	SC093121 Sequence
694	60.2	10.6	1104	6	AF047611	AF047611 Eurog1lyph	767	60.2	10.5	60	6	COS25290	COS25290 Sequence
695	60.2	10.6	1104	6	BD215254	BD215254 Novel hum	768	60.2	10.5	155	6	COS22591	COS22591 Sequence
696	60.2	10.6	1164	6	AX098194	AX098194 Sequence	769	60.2	10.5	185	6	AX425282	AX425282 Sequence
697	60.2	10.6	1178	6	BD275922	BD275922 Uncouplin	770	60.2	10.5	185	6	AX985976	AX985976 Sequence
698	60.2	10.6	1208	4	AB090246	AB090246 Pellic cat	771	60.2	10.5	185	6	BD120835	BD120835 Sequence
699	60.2	10.6	1320	5	BC067193	BC067193 Danto rer	772	60.2	10.5	201	11	BV200252	BV200252 Sequence
700	60.2	10.6	1510	9	BC037352	BC037352 Homo sapi	773	60.2	10.5	251	6	BD213305	BD213305 Sequence
701	60.2	10.6	1546	9	BC076399	BC076399 Homo sapi	774	60.2	10.5	348	6	CO671282	CO671282 Sequence
702	60.2	10.6	1572	9	BC044227	BC044227 Homo sapi	775	60.2	10.5	357	6	COS24729	COS24729 Sequence
703	60.2	10.6	1579	9	BC002809	BC002809 Homo sapi	776	60.2	10.5	396	6	CO481648	CO481648 Sequence
704	60.2	10.6	1697	10	AF166267	AF166267 Rattus no	777	60.2	10.5	418	6	COS26599	COS26599 Sequence
705	60.2	10.6	1717	5	BC065558	BC065558 Danto rer	778	60.2	10.5	437	6	COS27330	COS27330 Sequence
706	60.2	10.6	1718	9	BC073809	BC073809 Homo sapi	779	60.2	10.5	442	6	COS502790	COS502790 Sequence
707	60.2	10.6	1719	9	BC017498	BC017498 Homo sapi	780	60.2	10.5	442	6	COS51647	COS51647 Sequence
708	60.2	10.6	1723	9	BC047320	BC047320 Homo sapi	781	60.2	10.5	484	6	COS27337	COS27337 Sequence
709	60.2	10.6	1723	5	BC053112	BC053112 Danto rer	782	60.2	10.5	549	9	BC045165	BC045165 Homo sapi
710	60.2	10.6	1769	6	BD205071	BD205071 Human nuc	783	60.2	10.5	559	9	BC055570	BC055570 Homo sapi
711	60.2	10.6	1769	6	AX014293	AX014293 Sequence	784	60.2	10.5	555	5	BC05580	BC05580 Danto rer
712	60.2	10.6	1769	6	AX014293	AX014293 Sequence	785	60.2	10.5	757	3	AY241961	AY241961 Dementac
713	60.2	10.6	1769	6	AX014293	AX014293 Sequence	786	60.2	10.5	768	6	CO432402	CO432402 Sequence
714	60.2	10.6	1827	10	BC064057	BC064057 Mus muscu	787	60.2	10.5	814	10	RATPHGP	RATPHGP Sequence
715	60.2	10.6	1827	10	BC061765	BC061765 Rattus no	788	60.2	10.5	825	6	CO430950	CO430950 Sequence
716	60.2	10.6	1928	9	BC014402	BC014402 Homo sapi	789	60.2	10.5	873	6	AX780227	AX780227 Sequence
717	60.2	10.6	1928	9	BC041625	BC041625 Homo sapi	790	60.2	10.5	874	6	CO414670	CO414670 Sequence
718	60.2	10.6	1930	9	BC062575	BC062575 Homo sapi	791	60.2	10.5	875	9	BC001470	BC001470 Sequence
719	60.2	10.6	1999	9	BC020684	BC020684 Homo sapi	792	60.2	10.5	896	9	BC002491	BC002491 Sequence
720	60.2	10.6	2010	6	BD270044	BD270044 Secretd	793	60.2	10.5	1044	10	BC049565	BC049565 Homo sapi
721	60.2	10.6	2030	9	BC064537	BC064537 Homo sapi	794	60.2	10.5	1046	9	BC032585	BC032585 Mus muscu
722	60.2	10.6	2030	9	BC062592	BC062592 Homo sapi	795	60.2	10.5	1064	9	BC017344	BC017344 Homo sapi
723	60.2	10.6	2088	9	BC001045	BC001045 Homo sapi	796	60.2	10.5	1244	5	BC057461	BC057461 Sequence
724	60.2	10.6	2089	6	CQ774671	CQ774671 Sequence	797	60.2	10.5	1258	5	AX546767	AX546767 Danto rer
725	60.2	10.6	2089	9	BC016840	BC016840 Homo sapi	798	60.2	10.5	1263	6	AX047862	AX047862 Homo sapi
726	60.2	10.6	2220	9	AF132730	AF132730 Homo sapi	799	60.2	10.5	1290	9	BC002975	BC002975 Sequence
727	60.2	10.6	2225	9	AB063079	AB063079 Macaca fa	800	60.2	10.5	1325	6	AR034830	AR034830 Homo sapi
728	60.2	10.6	2295	9	BC062628	BC062628 Homo sapi	801	60.2	10.5	1325	6	AR093073	AR093073 Sequence
729	60.2	10.6	2312	9	HSM80373	HSM80373 Homo sapi	802	60.2	10.5	1325	6	CO875289	CO875289 Sequence
730	60.2	10.6	2351	9	BC051841	BC051841 Homo sapi	803	60.2	10.5	1325	6	196214	196214 Sequence
731	60.2	10.6	2369	9	AK074384	AK074384 Homo sapi	804	60.2	10.5	1325	6	AX587540	AX587540 Sequence
732	60.2	10.6	2409	9	BC049325	BC049325 Homo sapi	805	60.2	10.5	1325	6	AX695354	AX695354 Sequence
733	60.2	10.6	2446	9	BC039899	BC039899 Homo sapi	806	60.2	10.5	1325	6	BD079952	BD079952 Use relat
734	60.2	10.6	2614	9	BC042629	BC042629 Homo sapi	807	60.2	10.5	1325	6	HUMCYCD1	HUMCYCD1 Human cycli
735	60.2	10.6	2664	10	AY438023	AY438023 Mus muscu	808	60.2	10.5	1423	10	109360	109360 Sequence
736	60.2	10.6	2692	10	AY438023	AY438023 Mus muscu	809	60.2	10.5	1470	10	BC082085	BC082085 Rattus no
737	60.2	10.6	2699	6	CO801921	CO801921 Sequence	810	60.2	10.5	1521	9	BC031399	BC031399 Homo sapi
738	60.2	10.6	2725	5	BC077764	BC077764 Xenuptus t	811	60.2	10.5	1521	5	BC067689	BC067689 Danto rer
739	60.2	10.6	2725	5	BC077764	BC077764 Xenuptus t	812	60.2	10.5	1521	5	BC067689	BC067689 Danto rer
740	60.2	10.6	2809	9	BC032502	BC032502 Homo sapi	813	60.2	10.5	1625	9	BC004314	BC004314 Homo sapi
741	60.2	10.6	2872	10	BC049090	BC049090 Mus muscu	814	60.2	10.5	1625	10	AF089818	AF089818 Mus muscu
742	60.2	10.6	2920	9	BC063008	BC063008 Homo sapi	815	60.2	10.5	1629	10	BC033451	BC033451 Mus muscu
743	60.2	10.6	2920	9	BC063008	BC063008 Homo sapi	816	60.2	10.5	1643	10	BC024405	BC024405 Mus muscu
744	60.2	10.6	2989	5	AF171943	AF171943 Gallus ga	817	60.2	10.5	1749	9	BC057688	BC057688 Mus muscu
745	60.2	10.6	3019	10	BSM807541	BSM807541 Homo sapi	818	60.2	10.5	1842	9	AK026885	AK026885 Homo sapi
746	60.2	10.6	3121	9	BC007903	BC007903 Homo sapi	819	60.2	10.5	1905	9	BC032703	BC032703 Homo sapi
747	60.2	10.6	3144	5	BC068213	BC068213 Xenopus t	820	60.2	10.5	1910	9	BC043519	BC043519 Homo sapi
748	60.2	10.6	3172	9	BC027998	BC027998 Homo sapi	821	60.2	10.5	1935	9	BC015582	BC015582 Homo sapi
749	60.2	10.6	3220	9	BC064576	BC064576 Homo sapi	822	60.2	10.5	1964	6	AX795328	AX795328 Sequence

823	60	10.5	2084	5	BC080960	BC080960 Xenopus t	896	59.8	10.5	1073	10	BC035490	BC035490 Mus muscu
824	60	10.5	2166	5	BC082654	BC082654 Xenopus 1	897	59.8	10.5	1091	9	BC044230	BC044230 Homo sapi
825	60	10.5	2293	9	BC043566	BC043566 Homo sapi	898	59.8	10.5	1092	9	BC064140	BC064140 Homo sapi
826	60	10.5	2296	9	BC044946	BC044946 Homo sapi	899	59.8	10.5	1116	9	BC039532	BC039532 Homo sapi
827	60	10.5	2347	9	BC025927	BC025927 Homo sapi	900	59.8	10.5	1126	9	BC009010	BC009010 Homo sapi
828	60	10.5	2489	10	BC031749	BC031749 Mus muscu	901	59.8	10.5	1152	6	BD191482	BD191482 Secretd
829	60	10.5	2649	9	BC063539	BC063539 Homo sapi	902	59.8	10.5	1171	9	BC056889	BC056889 Homo sapi
830	60	10.5	2776	9	BSM803693	AL832385 Homo sapi	903	59.8	10.5	1302	4	AF244915	AF244915 Canis fam
831	60	10.5	2849	9	BC027241	BC027241 Homo sapi	904	59.8	10.5	1302	6	BD211567	BD211567 Canine an
832	60	10.5	2977	9	BC067260	BC067260 Homo sapi	905	59.8	10.5	1302	6	BD211568	BD211568 Canine an
833	60	10.5	3010	6	AX358754	AX358754 Sequence	906	59.8	10.5	1302	6	AR241545	AR241545 Sequence
834	60	10.5	3010	6	AX362247	AX362247 Sequence	c 907	59.8	10.5	1302	6	AR241546	AR241546 Sequence
835	60	10.5	3010	6	AX358753	AX358753 Homo sapi	908	59.8	10.5	1302	6	AR254501	AR254501 Sequence
836	60	10.5	3072	3	AK116778	AK116778 Homo sapi	c 909	59.8	10.5	1302	6	AR254502	AR254502 Sequence
837	60	10.5	3072	3	AK116778	AK116778 Rattus no	c 910	59.8	10.5	1307	6	BC023632	BC023632 Homo sapi
838	60	10.5	3567	10	BC057551	BC057551 Mus muscu	911	59.8	10.5	1319	6	AX337799	AX337799 Sequence
839	60	10.5	3606	9	AY078404	AY078404 Homo sapi	912	59.8	10.5	1319	6	AX779892	AX779892 Sequence
840	60	10.5	3625	10	BC064810	BC064810 Mus muscu	913	59.8	10.5	1319	6	HMTRNSAL	BC061713 Rattus no
841	60	10.5	3658	9	BSM803139	AL831825 Homo sapi	914	59.8	10.5	1330	10	BC061713	BC061713 Rattus no
842	60	10.5	3669	9	BSM805593	AL834206 Homo sapi	915	59.8	10.5	1359	10	MUSHAPTGB	L10353 Mus saxicol
843	60	10.5	3702	9	BC071612	BC071612 Homo sapi	916	59.8	10.5	1371	9	BC005805	BC005805 Homo sapi
844	60	10.5	3797	5	BC063922	BC063922 Xenopus t	917	59.8	10.5	1455	10	BC062408	BC062408 Rattus no
845	60	10.5	3844	10	BC056387	BC056387 Mus muscu	918	59.8	10.5	1480	5	BC062383	BC062383 Danio rer
846	60	10.5	3951	9	BC035812	BC035812 Homo sapi	919	59.8	10.5	1516	6	E02253	E02253 human 'A my
847	60	10.5	3993	10	BC060090	BC060090 Mus muscu	920	59.8	10.5	1525	10	BC048821	BC048821 Mus muscu
848	60	10.5	4017	10	BC066066	BC066066 Mus muscu	921	59.8	10.5	1562	3	AK115546	AK115546 Clona int
849	60	10.5	4631	10	BC057342	BC057342 Mus muscu	922	59.8	10.5	1606	9	BSM800215	BSM800215 Homo sapi
850	60	10.5	88306	8	NCEBK22	AL670543 Neurospor	923	59.8	10.5	1607	9	BC025369	BC025369 Homo sapi
c 851	60	10.5	193802	2	AC021133	AC021133 Homo sapi	924	59.8	10.5	1622	9	BC075857	BC075857 Homo sapi
852	60	10.5	292420	2	AC020873	AC020873 Mus muscu	925	59.8	10.5	1631	10	BC048708	BC048708 Mus muscu
853	59.8	10.5	135	6	AR419590	AR419590 Sequence	926	59.8	10.5	1635	9	BC017004	BC017004 Homo sapi
854	59.8	10.5	135	6	AX980284	AX980284 Sequence	927	59.8	10.5	1640	9	BC032422	BC032422 Homo sapi
855	59.8	10.5	135	6	BD115143	BD115143 EST and e	928	59.8	10.5	1641	9	BC017444	BC017444 Homo sapi
856	59.8	10.5	142	6	AR419304	AR419304 Sequence	929	59.8	10.5	1643	9	BC050730	BC050730 Homo sapi
857	59.8	10.5	142	6	AX979998	AX979998 Sequence	930	59.8	10.5	1658	5	BC047845	BC047845 Danio rer
858	59.8	10.5	146	6	BD114857	BD114857 EST and e	931	59.8	10.5	1662	9	BSM805109	BSM805109 Homo sapi
859	59.8	10.5	160	6	AR418838	AR418838 Sequence	932	59.8	10.5	1663	9	BC006481	BC006481 Homo sapi
860	59.8	10.5	160	6	AX979532	AX979532 Sequence	933	59.8	10.5	1666	9	BC001128	BC001128 Homo sapi
861	59.8	10.5	160	6	BD114391	BD114391 EST and e	934	59.8	10.5	1711	10	RNHIOSH1	X70685 R. norvegicu
862	59.8	10.5	163	6	AR418111	AR418111 Sequence	935	59.8	10.5	1768	9	BC073828	BC073828 Homo sapi
863	59.8	10.5	163	6	AX978805	AX978805 Sequence	936	59.8	10.5	1783	5	AF203473	AF203473 Salvelinu
864	59.8	10.5	163	6	BD113664	BD113664 EST and e	937	59.8	10.5	1795	5	BC064225	BC064225 Xenopus t
c 865	59.8	10.5	198	6	AX080530	AX080530 Sequence	938	59.8	10.5	1811	6	CO414890	CO414890 Sequence
866	59.8	10.5	220	6	CO488023	CO488023 Sequence	939	59.8	10.5	1820	9	BC065221	BC065221 Homo sapi
867	59.8	10.5	241	6	CO525819	CO525819 Sequence	940	59.8	10.5	1849	5	BC061396	BC061396 Xenopus t
868	59.8	10.5	274	6	CO522575	CO522575 Sequence	941	59.8	10.5	1897	5	BC049511	BC049511 Danio rer
869	59.8	10.5	304	6	CO487552	CO487552 Sequence	942	59.8	10.5	1920	3	AY061375	AY061375 Drosophill
870	59.8	10.5	315	6	CO517813	CO517813 Sequence	943	59.8	10.5	1942	10	BC071268	BC071268 Mus muscu
871	59.8	10.5	338	6	CO522686	CO522686 Sequence	944	59.8	10.5	1950	9	BC028206	BC028206 Homo sapi
c 872	59.8	10.5	360	6	CO427909	CO427909 Sequence	945	59.8	10.5	1990	9	AK000212	AK000212 Homo sapi
873	59.8	10.5	425	6	CO524522	CO524522 Sequence	946	59.8	10.5	2005	9	BSM803426	BSM803426 Homo sapi
874	59.8	10.5	479	9	BC040728	BC040728 Homo sapi	947	59.8	10.5	2054	9	BC058863	BC058863 Homo sapi
875	59.8	10.5	485	10	BC022770	BC022770 Mus muscu	948	59.8	10.5	2090	9	BC020565	BC020565 Homo sapi
c 876	59.8	10.5	541	6	CO411393	CO411393 Sequence	949	59.8	10.5	2127	5	BC071276	BC071276 Danio rer
877	59.8	10.5	589	10	BC002135	BC002135 Mus muscu	950	59.8	10.5	2170	9	AK074292	AK074292 Homo sapi
878	59.8	10.5	607	5	BC049055	BC049055 Danio rer	951	59.8	10.5	2174	10	BC0044798	BC0044798 Mus muscu
c 879	59.8	10.5	608	6	CO410246	CO410246 Sequence	952	59.8	10.5	2183	9	BC025699	BC025699 Homo sapi
c 880	59.8	10.5	664	6	CO376688	CO376688 Sequence	953	59.8	10.5	2208	10	BC052821	BC052821 Mus muscu
c 881	59.8	10.5	664	6	CO403965	CO403965 Sequence	954	59.8	10.5	2211	9	BC033795	BC033795 Homo sapi
882	59.8	10.5	716	9	BC044236	BC044236 Homo sapi	955	59.8	10.5	2220	5	BC067610	BC067610 Danio rer
883	59.8	10.5	732	6	BD191101	BD191101 186 human	956	59.8	10.5	2332	9	BSM803479	BSM803479 Homo sapi
884	59.8	10.5	732	6	AX924611	AX924611 Sequence	957	59.8	10.5	2366	9	BC017481	BC017481 Homo sapi
885	59.8	10.5	760	5	CO497632	CO497632 Sequence	958	59.8	10.5	2420	9	BC072670	BC072670 Homo sapi
886	59.8	10.5	780	5	BC076636	BC076636 Xenopus t	959	59.8	10.5	2435	6	AX780077	AX780077 Sequenco
887	59.8	10.5	791	8	OSA004966	AJ0004966 Oryza sat	960	59.8	10.5	2446	9	BSM808753	BSM808753 Homo sapi
888	59.8	10.5	812	6	E15569	E15569 CDNA encodi	961	59.8	10.5	2475	3	AY296116	AY296116 Ixodes sc
889	59.8	10.5	812	6	AR222758	AR222758 Mus muscu	962	59.8	10.5	2522	10	BC0650505	BC0650505 Homo sapi
890	59.8	10.5	827	10	BC049739	BC049739 Mus muscu	963	59.8	10.5	2531	9	BC027040	BC027040 Homo sapi
891	59.8	10.5	883	10	BC049726	BC049726 Mus muscu	964	59.8	10.5	2534	10	BC066224	BC066224 Mus muscu
c 892	59.8	10.5	886	11	BV175306	BV175306 sqgm/8236	965	59.8	10.5	2575	6	BD140638	BD140638 36 human
c 893	59.8	10.5	911	9	BC004926	BC004926 Homo sapi	966	59.8	10.5	2575	6	AR409293	AR409293 Sequence
c 894	59.8	10.5	1066	6	AX285241	AX285241 Sequence	967	59.8	10.5	2584	6	BD140660	BD140660 36 human
895	59.8	10.5	1071	9	BC046244	BC046244 Homo sapi	968	59.8	10.5	2584	6	AR409315	AR409315 Sequence

969	59.8	10.5	2590	9	BC047315	1042	59.6	10.5	578	9	BC003052	BC003052 Homo sapi
970	59.8	10.5	2604	9	BC032396	c1043	59.6	10.5	645	9	CQ397628	CQ397628 Sequence
971	59.8	10.5	2652	3	AKI74388	c1044	59.6	10.5	645	6	CQ403927	CQ403927 Sequence
972	59.8	10.5	2681	10	BC064454	1045	59.6	10.5	651	10	BC038494	BC038494 Mus muscu
973	59.8	10.5	2713	9	BC021912	1046	59.6	10.5	716	9	BC015172	BC015172 Homo sapi
974	59.8	10.5	2756	9	BC025980	1047	59.6	10.5	814	10	BC025933	BC025933 Mus muscu
975	59.8	10.5	2840	10	BC052769	1048	59.6	10.5	847	9	BC053571	BC053571 Homo sapi
976	59.8	10.5	2859	10	BC031850	1049	59.6	10.5	882	6	AR487879	AR487879 Mus muscu
977	59.8	10.5	2880	6	BD270054	1050	59.6	10.5	901	5	BC082363	BC082363 Homo sapi
978	59.8	10.5	2954	6	AR564552	1051	59.6	10.5	916	6	CQ769319	CQ769319 Sequence
979	59.8	10.5	2979	9	BC031084	1052	59.6	10.5	1024	9	HSM806312	HSM806312 Homo sapi
980	59.8	10.5	3110	9	HSM803101	1053	59.6	10.5	1107	9	BC042635	BC042635 Homo sapi
981	59.8	10.5	3166	10	BC034110	1054	59.6	10.5	1117	9	BC040937	BC040937 Homo sapi
982	59.8	10.5	3186	5	BC068331	1055	59.6	10.5	1137	3	AKI16124	AKI16124 Homo sapi
983	59.8	10.5	3191	9	BC020095	1056	59.6	10.5	1198	6	AR105078	AR105078 Sequence
984	59.8	10.5	3197	5	BC054582	1057	59.6	10.5	1198	8	AR244677	AR244677 Zea mays
985	59.8	10.5	3211	10	BC055403	1058	59.6	10.5	1319	9	BC034528	BC034528 Homo sapi
986	59.8	10.5	3216	9	BC070047	1059	59.6	10.5	1362	5	BC054956	BC054956 Xenopus 1
987	59.8	10.5	3230	10	BC037665	1060	59.6	10.5	1366	9	BC063409	BC063409 Homo sapi
988	59.8	10.5	3245	9	HSM805849	1061	59.6	10.5	1490	9	BC053541	BC053541 Homo sapi
989	59.8	10.5	3260	10	BC083123	1062	59.6	10.5	1530	9	BC015917	BC015917 Homo sapi
990	59.8	10.5	3273	10	BC023693	1063	59.6	10.5	1587	9	BC067943	BC067943 Homo sapi
991	59.8	10.5	3298	9	AR453583	1064	59.6	10.5	1626	5	BC028121	BC028121 Homo sapi
992	59.8	10.5	3371	9	AR453583	1065	59.6	10.5	1652	9	BC062018	BC062018 Homo sapi
993	59.8	10.5	3390	9	BC042068	1066	59.6	10.5	1660	10	BC062018	BC062018 Homo sapi
994	59.8	10.5	3421	10	BC067203	1067	59.6	10.5	1720	10	BC052633	BC052633 Mus muscu
995	59.8	10.5	3425	5	BC072233	1068	59.6	10.5	1741	5	BC047856	BC047856 Danio rer
996	59.8	10.5	3596	9	HSM806341	1069	59.6	10.5	1787	9	BC031878	BC031878 Homo sapi
997	59.8	10.5	3788	10	BC022120	1070	59.6	10.5	1850	9	BC036918	BC036918 Homo sapi
998	59.8	10.5	3824	9	HSM805271	1071	59.6	10.5	1860	9	BC058897	BC058897 Homo sapi
999	59.8	10.5	3890	10	BC056382	1072	59.6	10.5	1870	9	BC048801	BC048801 Homo sapi
1000	59.8	10.5	4218	9	HSM807520	1073	59.6	10.5	1886	10	BC007146	BC007146 Mus muscu
1001	59.8	10.5	4329	9	BC071579	1074	59.6	10.5	1917	9	BC074287	BC074287 Homo sapi
1002	59.8	10.5	4399	9	BC048185	1075	59.6	10.5	1951	5	BC064630	BC064630 Danio rer
1003	59.8	10.5	4407	10	BC059794	1076	59.6	10.5	2159	6	AX285189	AX285189 Sequence
1004	59.8	10.5	4430	5	BC057791	1077	59.6	10.5	2190	9	BC048340	BC048340 Homo sapi
1005	59.8	10.5	4513	10	BC051030	1078	59.6	10.5	2270	9	BC062610	BC062610 Homo sapi
1006	59.8	10.5	4726	9	BC054543	1079	59.6	10.5	2549	10	BC032289	BC032289 Mus muscu
1007	59.8	10.5	4755	5	BC047162	1080	59.6	10.5	2633	9	HSM804706	HSM804706 Homo sapi
1008	59.8	10.5	4759	5	HSZPHSL2	1081	59.6	10.5	2660	5	BC064852	BC064852 Homo sapi
1009	59.8	10.5	4915	9	HSZPHSL2	1082	59.6	10.5	2667	9	BC004119	BC004119 Homo sapi
1010	59.8	10.5	5368	5	BC081553	1083	59.6	10.5	2702	9	BC014077	BC014077 Homo sapi
1011	59.8	10.5	5671	14	AB049089	1084	59.6	10.5	2725	9	BC032783	BC032783 Homo sapi
1012	59.8	10.5	5711	14	AB049089	1085	59.6	10.5	2787	9	BC008025	BC008025 Homo sapi
1013	59.8	10.5	5871	14	AB049089	1086	59.6	10.5	2792	9	BC075824	BC075824 Homo sapi
1014	59.8	10.5	5951	2	AC068715	1087	59.6	10.5	2916	6	BD275095	BD275095 Homo sapi
1015	59.8	10.5	5951	2	AC068715	1088	59.6	10.5	2989	10	BC058211	BC058211 Mus muscu
1016	59.8	10.5	5951	2	AC068715	1089	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1017	59.8	10.5	5951	2	AC068715	1090	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1018	59.8	10.5	5951	2	AC068715	1091	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1019	59.8	10.5	5951	2	AC068715	1092	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1020	59.8	10.5	5951	2	AC068715	1093	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1021	59.8	10.5	5951	2	AC068715	1094	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1022	59.8	10.5	5951	2	AC068715	1095	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1023	59.8	10.5	5951	2	AC068715	1096	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1024	59.8	10.5	5951	2	AC068715	1097	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1025	59.8	10.5	5951	2	AC068715	1098	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1026	59.8	10.5	5951	2	AC068715	1099	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1027	59.8	10.5	5951	2	AC068715	1100	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1028	59.8	10.5	5951	2	AC068715	1101	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1029	59.8	10.5	5951	2	AC068715	1102	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1030	59.8	10.5	5951	2	AC068715	1103	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1031	59.8	10.5	5951	2	AC068715	1104	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1032	59.8	10.5	5951	2	AC068715	1105	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1033	59.8	10.5	5951	2	AC068715	1106	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1034	59.8	10.5	5951	2	AC068715	1107	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1035	59.8	10.5	5951	2	AC068715	1108	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1036	59.8	10.5	5951	2	AC068715	1109	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1037	59.8	10.5	5951	2	AC068715	1110	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1038	59.8	10.5	5951	2	AC068715	1111	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1039	59.8	10.5	5951	2	AC068715	1112	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1040	59.8	10.5	5951	2	AC068715	1113	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1041	59.8	10.5	5951	2	AC068715	1114	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi
1042	59.8	10.5	5951	2	AC068715	1115	59.6	10.5	3145	6	BD275095	BD275095 Homo sapi

1115	59.4	10.4	146	6	AX985892	Sequence	1188	59.4	10.4	2789	10	BC050830	BC050830 Mus muscu
1116	59.4	10.4	146	6	BD120742	EST and e	1189	59.4	10.4	2841	10	BC045601	BC045601 Mus muscu
1117	59.4	10.4	146	6	BD120751	EST and e	1190	59.4	10.4	2851	9	BC021117	BC021117 Homo sapi
1118	59.4	10.4	169	6	AR419752	Sequence	1191	59.4	10.4	3004	9	BC064983	BC064983 Homo sapi
1119	59.4	10.4	169	6	AX980446	Sequence	1192	59.4	10.4	3080	6	AR183238	AR183238 Sequence
1120	59.4	10.4	169	6	BD115305	EST and e	1193	59.4	10.4	3080	6	AR205638	AR205638 Sequence
1121	59.4	10.4	179	6	AR418078	Sequence	1194	59.4	10.4	3080	6	AR241240	AR241240 Sequence
1122	59.4	10.4	179	6	AX978772	Sequence	1195	59.4	10.4	3080	6	AR256256	AR256256 Sequence
1123	59.4	10.4	179	6	BD113631	EST and e	1196	59.4	10.4	3080	6	AR391603	AR391603 Sequence
1124	59.4	10.4	201	11	BV204551	Sequence	1197	59.4	10.4	3080	6	AX082223	AX082223 Sequence
1125	59.4	10.4	237	6	AX284920	Sequence	1198	59.4	10.4	3080	6	BD124002	BD124002 Novel mol
1126	59.4	10.4	244	6	AX201931	Sequence	1199	59.4	10.4	3121	6	AX046405	AX046405 Sequence
1127	59.4	10.4	299	6	C0526545	Sequence	1200	59.4	10.4	3121	6	BC014305	BC014305 Homo sapi
1128	59.4	10.4	341	6	C0522918	Sequence	1201	59.4	10.4	3642	10	BC053385	BC053385 Mus muscu
1129	59.4	10.4	364	3	AF163972	Taenia so	1202	59.4	10.4	3660	9	BC035683	BC035683 Homo sapi
1130	59.4	10.4	372	3	AF216695	Taenia so	1203	59.4	10.4	4142	10	BC053026	BC053026 Mus muscu
1131	59.4	10.4	372	10	BC027531	Mus muscu	1204	59.4	10.4	4158	9	HSW805995	BS575714 Homo sapi
1132	59.4	10.4	383	6	C0525716	Sequence	1205	59.4	10.4	4438	10	BC067016	BS577490 Homo sapi
1133	59.4	10.4	450	10	BC083104	Mus muscu	1206	59.4	10.4	5309	6	HSW805828	AX345714 Sequence
1134	59.4	10.4	476	6	C0410349	Sequence	1207	59.4	10.4	6059	6	AX345714	AX345714 Sequence
1135	59.4	10.4	550	10	BC024397	Mus muscu	1208	59.4	10.4	6577	6	AX351920	AX351920 Sequence
1136	59.4	10.4	664	6	BD231009	49 human	1209	59.4	10.4	6577	6	AX346258	AX346258 Sequence
1137	59.4	10.4	664	6	AR337304	Sequence	1210	59.4	10.4	6577	6	AX348993	AX348993 Sequence
1138	59.4	10.4	761	6	BD019227	Novel gen	1211	59.4	10.4	7930	9	HSW808084	BS647938 Homo sapi
1139	59.4	10.4	761	6	BD099165	Novel gen	1212	59.4	10.4	8765	2	AC008477	AC008477 Homo sapi
1140	59.4	10.4	868	9	BC065714	Homo sapi	1213	59.4	10.4	110000	2	AC116984_2	Continuation (3 of
1141	59.4	10.4	956	9	BC003637	Homo sapi	1214	59.4	10.4	112643	2	AC009187	Continuation (3 of
1142	59.4	10.4	965	6	C0776429	Sequence	1215	59.4	10.4	118119	10	AL807243	AL807243 Mouse DNA
1143	59.4	10.4	996	10	BC032292	Mus muscu	1216	59.4	10.4	166555	2	AC141826	AC141826 Apis mell
1144	59.4	10.4	1001	10	BC049605	Mus muscu	1217	59.4	10.4	167120	10	AC110178	AC110178 Mus muscu
1145	59.4	10.4	1019	5	BC084449	Xenopus t	1218	59.4	10.4	168721	9	AC136431	AC136431 Homo sapi
1146	59.4	10.4	1029	9	BC029872	Homo sapi	1219	59.4	10.4	170861	2	AC025698	AC025698 Homo sapi
1147	59.4	10.4	1080	9	BC022354	Homo sapi	1220	59.4	10.4	173113	2	AC138982	AC138982 Homo sapi
1148	59.4	10.4	1083	5	BC061302	Xenopus t	1221	59.4	10.4	195740	2	AC141269	AC141269 Homo sapi
1149	59.4	10.4	1119	9	BC070137	Homo sapi	1222	59.4	10.4	235592	2	AC110436	AC110436 Rattus no
1150	59.4	10.4	1131	9	BC004252	Homo sapi	1223	59.4	10.4	244215	2	AC095004	AC095004 Rattus no
1151	59.4	10.4	1202	3	AY122189	Drosophil	1224	59.4	10.4	250565	2	CR318655	CR318655 Danio rer
1152	59.4	10.4	1222	9	AF110329	Homo sapi	1225	59.4	10.4	252504	2	AC073815	AC073815 Mus muscu
1153	59.4	10.4	1255	9	BC042461	Homo sapi	1226	59.4	10.4	154	6	AX381214	AX381214 Sequence
1154	59.4	10.4	1259	6	E03348	CDNA sequen	1227	59.4	10.4	165	6	AR416630	AR416630 Sequence
1155	59.4	10.4	1358	5	BC044957	Xenopus t	1228	59.4	10.4	165	6	AY977324	AY977324 Sequence
1156	59.4	10.4	1375	10	RNP3PROT	Rattus rat	1229	59.4	10.4	165	6	BD112183	BD112183 EST and e
1157	59.4	10.4	1388	3	AY069347	Drosophil	1230	59.4	10.4	176	6	C05677241	C05677241 Sequence
1158	59.4	10.4	1416	5	AF090943	Homo sapi	1231	59.4	10.4	204	6	C0525707	C0525707 Sequence
1159	59.4	10.4	1426	5	BC054250	Xenopus t	1232	59.4	10.4	209	6	C0525608	C0525608 Sequence
1160	59.4	10.4	1449	3	BT011495	Drosophil	1233	59.4	10.4	212	6	C0677317	C0677317 Sequence
1161	59.4	10.4	1680	5	BC056749	Danio rer	1234	59.4	10.4	224	6	C0526058	C0526058 Sequence
1162	59.4	10.4	1688	10	BC005523	Mus muscu	1235	59.4	10.4	252	6	C0526702	C0526702 Sequence
1163	59.4	10.4	1692	5	BC045295	Danio rer	1236	59.4	10.4	258	6	AR423856	AR423856 Sequence
1164	59.4	10.4	1733	10	BC083553	Rattus no	1237	59.4	10.4	258	6	AX984550	AX984550 Sequence
1165	59.4	10.4	1749	10	BC046612	Mus muscu	1238	59.4	10.4	258	6	BD119409	BD119409 EST and e
1166	59.4	10.4	1820	6	AX593406	Sequence	1239	59.4	10.4	265	6	C0526081	C0526081 Sequence
1167	59.4	10.4	1832	5	BC080902	Xenopus t	1240	59.4	10.4	267	6	C0410745	C0410745 Sequence
1168	59.4	10.4	1931	6	C0498497	Sequence	1241	59.4	10.4	268	6	C0525997	C0525997 Sequence
1169	59.4	10.4	1938	6	C0412894	Sequence	1242	59.4	10.4	268	6	C0526263	C0526263 Sequence
1170	59.4	10.4	1938	10	BC079260	Rattus no	1243	59.4	10.4	274	6	C0526796	C0526796 Sequence
1171	59.4	10.4	1962	9	BC058882	Homo sapi	1244	59.4	10.4	284	6	C0526203	C0526203 Sequence
1172	59.4	10.4	1999	9	BC006527	Homo sapi	1245	59.4	10.4	284	6	C0526722	C0526722 Sequence
1173	59.4	10.4	2042	9	AK027146	Homo sapi	1246	59.4	10.4	312	6	C0525834	C0525834 Sequence
1174	59.4	10.4	2051	6	AX780311	Sequence	1247	59.4	10.4	323	6	C0524910	C0524910 Sequence
1175	59.4	10.4	2054	6	AX663299	Sequence	1248	59.4	10.4	356	6	C0517353	C0517353 Sequence
1176	59.4	10.4	2130	10	BC062005	Rattus no	1249	59.4	10.4	380	6	C0526811	C0526811 Sequence
1177	59.4	10.4	2135	9	BC056757	Homo sapi	1250	59.4	10.4	391	6	C0524976	C0524976 Sequence
1178	59.4	10.4	2161	9	AB063084	Macaca fa	1251	59.4	10.4	401	6	C0522435	C0522435 Sequence
1179	59.4	10.4	2195	9	BC042607	Homo sapi	1252	59.4	10.4	402	6	C0411023	C0411023 Sequence
1180	59.4	10.4	2195	9	BC044936	Homo sapi	1253	59.4	10.4	410	10	BC044054	BC044054 Mus muscu
1181	59.4	10.4	2235	9	BC017301	Homo sapi	1254	59.4	10.4	426	9	HSW802848	AL512719 Homo sapi
1182	59.4	10.4	2236	9	BC000317	Homo sapi	1255	59.4	10.4	433	6	C0526050	AL512719 Homo sapi
1183	59.4	10.4	2230	9	BC036827	Homo sapi	1256	59.4	10.4	436	6	C0522487	C0522487 Sequence
1184	59.4	10.4	2252	9	AB063071	Macaca fa	1257	59.4	10.4	437	6	C0520397	C0520397 Sequence
1185	59.4	10.4	2570	10	BC037607	Mus muscu	1258	59.4	10.4	444	6	BC002750	BC002750 Homo sapi
1186	59.4	10.4	2581	9	BC031820	Homo sapi	1259	59.4	10.4	448	6	C0525199	C0525199 Sequence
1187	59.4	10.4	2584	9	HSW808543	Homo sapi	1260	59.4	10.4	453	6	C0526678	C0526678 Sequence

1261	59.2	10.4	458	9	BSM806076	1334	59.2	10.4	2884	9	BSM807509	BX647066 Homo sapi
1262	59.2	10.4	476	6	CQ526175	1335	59.2	10.4	3021	9	BC033086	BC033086 Homo sapi
1263	59.2	10.4	489	6	CQ524523	1336	59.2	10.4	3084	9	BC025782	BC025782 Homo sapi
1264	59.2	10.4	490	6	CQ526663	1337	59.2	10.4	3255	5	BC068362	BC068362 Homo sapi
1265	59.2	10.4	509	6	CQ522420	1338	59.2	10.4	3255	5	BC068362	BC068362 Homo sapi
1266	59.2	10.4	510	6	CQ526266	1339	59.2	10.4	3479	9	BSM800673	BSM800673 Homo sapi
1267	59.2	10.4	532	6	CQ525634	1340	59.2	10.4	3532	9	BSM807375	BSM807375 Homo sapi
1268	59.2	10.4	541	6	BC038211	1341	59.2	10.4	3558	10	BC031201	BC031201 Homo sapi
1269	59.2	10.4	549	6	CQ526150	1342	59.2	10.4	3559	9	BC028100	BC028100 Homo sapi
C1270	59.2	10.4	566	6	CQ410439	1343	59.2	10.4	4064	6	AR526951	AR526951 Homo sapi
1271	59.2	10.4	579	6	CQ526139	1344	59.2	10.4	4146	9	AR538405	AR538405 Homo sapi
1272	59.2	10.4	585	6	CQ526237	1345	59.2	10.4	4295	10	BSM805210	BSM805210 Homo sapi
1273	59.2	10.4	627	10	BC061005	1346	59.2	10.4	4518	9	BSM802971	BSM802971 Homo sapi
1274	59.2	10.4	645	6	CQ769291	1347	59.2	10.4	4636	10	BC057352	BC057352 Homo sapi
1275	59.2	10.4	704	10	BC049749	1348	59.2	10.4	4779	3	AB120954	AB120954 Homo sapi
1276	59.2	10.4	722	5	BD192304	1349	59.2	10.4	5359	10	BC054082	BC054082 Homo sapi
1277	59.2	10.4	779	5	BC076202	1350	59.2	10.4	65076	8	NCB13020	NCB13020 Homo sapi
1278	59.2	10.4	837	9	S78214	1351	59.2	10.4	126611	10	AL928592	AL928592 Homo sapi
1279	59.2	10.4	975	10	BC012263	1352	59.2	10.4	134218	2	HS17085	HS17085 Homo sapi
1280	59.2	10.4	982	9	BC022482	1353	59.2	10.4	170655	2	AP001012	AP001012 Homo sapi
1281	59.2	10.4	1014	9	BC016845	1354	59.2	10.4	188873	2	AC019223	AC019223 Homo sapi
1282	59.2	10.4	1048	9	BC063640	1355	59.2	10.4	196754	2	BX957296	BX957296 Homo sapi
1283	59.2	10.4	1065	10	BC026521	1356	59.2	10.4	200441	2	AC022130	AC022130 Homo sapi
1284	59.2	10.4	1122	9	BC046132	1357	59.2	10.4	216410	2	AC027321	AC027321 Homo sapi
1285	59.2	10.4	1128	9	BC071732	1358	59.2	10.4	260	6	CQ524964	CQ524964 Homo sapi
1286	59.2	10.4	1160	9	BC035911	1359	59.2	10.4	260	6	CQ525782	CQ525782 Homo sapi
1287	59.2	10.4	1178	10	BC018244	1360	59.2	10.4	270	6	AR426430	AR426430 Homo sapi
1288	59.2	10.4	1204	6	AX040958	1361	59.2	10.4	270	6	AR426430	AR426430 Homo sapi
1289	59.2	10.4	1324	10	BC013526	1362	59.2	10.4	270	6	AR426430	AR426430 Homo sapi
1290	59.2	10.4	1409	10	BC013526	1363	59.2	10.4	270	6	AR426430	AR426430 Homo sapi
1291	59.2	10.4	1425	5	BC074593	1364	59.2	10.4	285	6	BD121983	BD121983 Homo sapi
1292	59.2	10.4	1464	9	BC021958	1365	59.2	10.4	291	6	CQ523667	CQ523667 Homo sapi
1293	59.2	10.4	1497	9	BC042061	1366	59.2	10.4	305	6	CQ522628	CQ522628 Homo sapi
1294	59.2	10.4	1513	8	AP169799	1367	59.2	10.4	305	6	CQ524005	CQ524005 Homo sapi
1295	59.2	10.4	1576	9	BC000253	1368	59.2	10.4	313	6	CQ523441	CQ523441 Homo sapi
1296	59.2	10.4	1590	9	BSM803698	1369	59.2	10.4	321	6	CQ524273	CQ524273 Homo sapi
1297	59.2	10.4	1624	9	BC064422	1370	59.2	10.4	376	6	CQ525261	CQ525261 Homo sapi
1298	59.2	10.4	1638	10	BC026670	1371	59.2	10.4	387	6	CQ522618	CQ522618 Homo sapi
1299	59.2	10.4	1684	10	BC055910	1372	59.2	10.4	409	10	RMNTCYTOX	RMNTCYTOX Homo sapi
1300	59.2	10.4	1719	5	BC063347	1373	59.2	10.4	424	6	CQ523864	CQ523864 Homo sapi
1301	59.2	10.4	1731	9	BC062328	1374	59.2	10.4	431	6	CQ524328	CQ524328 Homo sapi
1302	59.2	10.4	1767	9	BSM800099	1375	59.2	10.4	432	6	CQ524164	CQ524164 Homo sapi
1303	59.2	10.4	1785	5	BC067644	1376	59.2	10.4	439	6	CQ522595	CQ522595 Homo sapi
1304	59.2	10.4	1835	10	BC002047	1377	59.2	10.4	439	6	CQ522546	CQ522546 Homo sapi
1305	59.2	10.4	1852	9	BC032623	1378	59.2	10.4	441	3	AK174241	AK174241 Homo sapi
1306	59.2	10.4	1865	10	BC013463	1379	59.2	10.4	466	6	CQ522677	CQ522677 Homo sapi
1307	59.2	10.4	1872	10	BC033437	1380	59.2	10.4	473	6	CQ523433	CQ523433 Homo sapi
1308	59.2	10.4	1877	5	BC077826	1381	59.2	10.4	490	6	CQ523744	CQ523744 Homo sapi
1309	59.2	10.4	1880	9	BC051816	1382	59.2	10.4	502	6	CQ522371	CQ522371 Homo sapi
1310	59.2	10.4	1914	6	A49139	1383	59.2	10.4	511	6	CQ525377	CQ525377 Homo sapi
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1312	59.2	10.4	1940	6	BC035627	1385	59.2	10.4	532	10	BC049701	BC049701 Homo sapi
1313	59.2	10.4	1940	6	BC064004	1386	59.2	10.4	575	10	BC028505	BC028505 Homo sapi
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1412	59	10.4	1271	5	BC053296	BC053296 Danto rer
1413	59	10.4	1277	9	AB096984	AB096984 Macaca fa
1414	59	10.4	1310	9	BC065107	BC065107 Homo sapi
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1417	59	10.4	1376	3	AK174635	AK174635 Clona int
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1419	59	10.4	1436	9	BSM804685	BSM804685 Homo sapi
1420	59	10.4	1444	9	BC053609	BC053609 Homo sapi
1421	59	10.4	1495	5	BC046652	BC046652 Xenopus t
1422	59	10.4	1507	10	BC069867	BC069867 Mus muscu
1423	59	10.4	1510	9	BC062585	BC062585 Homo sapi
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1435	59	10.4	1792	10	BC027065	BC027065 Mus muscu
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1438	59	10.4	1814	3	AY118710	AY118710 Drosophi1
1439	59	10.4	1818	10	BC023454	BC023454 Mus muscu
1440	59	10.4	1847	6	AX795332	AX795332 Sequence
1441	59	10.4	1875	10	BC058247	BC058247 Mus muscu
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1446	59	10.4	1930	5	BC046873	BC046873 Danto rer
1447	59	10.4	1935	9	BC030246	BC030246 Homo sapi
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1449	59	10.4	1943	5	BC054628	BC054628 Danto rer
1450	59	10.4	1977	5	BC074690	BC074690 Xenopus t
1451	59	10.4	1988	10	BC028378	BC028378 Mus muscu
1452	59	10.4	2021	5	BC074652	BC074652 Xenopus t
1453	59	10.4	2022	9	AB061793	AB061793 Homo sapi
1454	59	10.4	2064	9	BC033388	BC033388 Homo sapi
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1456	59	10.4	2071	5	BC056843	BC056843 Xenopus t
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1460	59	10.4	2132	9	BC042102	BC042102 Homo sapi
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1462	59	10.4	2149	9	BC072428	BC072428 Homo sapi
1463	59	10.4	2181	9	BC009940	BC009940 Homo sapi
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1466	59	10.4	2237	3	AK112710	AK112710 Clona int
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1480	59	10.4	2596	9	BC052994	BC052994 Homo sapi
1481	59	10.4	2660	9	BC031405	BC031405 Homo sapi
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1486	59	10.4	2957	10	AJ609635	AJ609635 Mus muscu
1487	59	10.4	3149	10	BC040763	BC040763 Mus muscu
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1494	59	10.4	3566	9	BSM803611	BSM803611 Homo sapi
1495	59	10.4	3905	10	BC058357	BC058357 Mus muscu
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1498	59	10.4	5210	9	BSM803446	BSM803446 Homo sapi
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ALIGNMENTS

RESULT 1
AR252648
LOCUS AR252648 570 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 407 from patent US 6478825.
ACCESSION AR252648
VERSION AR252648.1 GI:27300556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 570)
Wintersbottom J.M., Shimp L., Boyce T.M. and Kaes D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
Patent: US 6478825-A 407 12-NOV-2002;
JOURNAL Location/Qualifiers
FEATURES
source
1..570
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ORIGIN

Query Match 100.0%; Score 570; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 6-9e-86;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGGAGGACCGGGATPAGAGCCTGCGCTTGTCCCGGCGACGCGCAGCTTCCCGCGC	60
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QY	61	GGCCCGAGCGCCCG	120
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QY	121	TTCAGCTCGCGCTGCTGCTTCTTATGAGGCGTGGCGCGCGCGCGCGCGCGCGCG	180
DB	121	TTCAGCTCGCGCTGCTGCTTCTTATGAGGCGTGGCGCGCGCGCGCGCGCGCGCG	180
QY	181	GGCGTGAAGTCG	240
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QY	301	TCCAGAGTGTGTGCTGAGCTGGGTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCG	360
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 QY 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570
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RESULT 2
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 LOCUS Sequence 407 from Patent WO0073454.
 DEFINITION AX403520
 ACCESSION AX403520.1 GI:21437002
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
 Ferrara, N., Gerber, H., Gertlisen, M., Goddard, A., Godowski, P.,
 Grimaldi, C.J., Gurney, A.L., Kijavich, I., Nader, M.A., Pan, J.,
 Paoli, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
 Williams, P., Wood, W.I. and Zhang, Z.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent WO 0073454-A 407 07-DEC-2000;
 Genentech Inc. (US)
 FEATURES
 source
 1. 570
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 100.0%; Score 570; DB 6; Length 570;
 Best Local Similarity 100.0%; Pred. No. 6.9e-86;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGAGCCGGTATTAAGAGCCTGCTGAGCTTGGCCGAGCAGCCGACGTTCCCGGCGC 60
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 QY 301 TCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCCTGAAGCCCTGAAG 360
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 QY 361 GCCCTGCTGGGGGCCCTGACAGTGTGTTGGCTGAGCCGAGACTGAGACATCTACACTGAG 420
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 Db 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570

RESULT 3
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 DEFINITION AY359064
 ACCESSION AY359064.1 GI:37183245
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 Clark, H.P., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, O., Hass, P.B.,
 Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, X., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simons, L., Singh, J., Smith, V.,
 Stinson, J., Vagstad, R., Vanden, R., Watanabe, C., Wiesend, D., Woods, K.,
 Xie, M.H., Yanstra, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
 Goddard, A., Wood, W.I. and Godowski, P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE
 AUTHORS
 2 (bases 1 to 570)
 Submitted Submission
 Title
 JOURNAL Direct Submission
 Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN
 Query Match 100.0%; Score 570; DB 9; Length 570;
 Best Local Similarity 100.0%; Pred. No. 6.9e-86;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Incyte Clone No: 3120415
FH Key Location/Qualifiers
FT source 1..543
FT Location/Qualifiers
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ORIGIN

Query Match 92.8%; Score 529; DB 6; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-79;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGGACCGGGTATTAAGAAAGCTCGTGGCTTGCCTCCGGGACGCGCAGATTCCCGCGC 60
DB 15 GCGAGGACCGGGTATTAAGAAAGCTCGTGGCTTGCCTCCGGGACGCGCAGATTCCCGCGC 74
QY 61 GCGCGAGCGCGGCGCATGAAGCTCGCGGCTCTGCGGAGCTGCGGCTGCTGCT 120
DB 75 GCGCGAGCGCGGCGCATGAAGCTCGCGGCTCTGCGGAGCTGCGGCTGCTGCT 134
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DB 255 AACCGCTGAAGCTCTGCTGAGCAGCTGGGATCCCGTGAACCACTCATAGAGGCG 314
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QY 361 GCCCTGCTGGGGGCGCTGACAGTGTGGTGAAGCGGAGCGGAGCTGACATCACTGAG 420
DB 375 GCCCTGCTGGGGGCGCTGACAGTGTGGTGAAGCGGAGCGGAGCTGACATCACTGAG 434
QY 421 GACAAAGCGCTGCGCAACCGCGAGGCGTGAACCCCGCGGAGGAGGAGCGTCCATCC 480
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DB 495 CTTTCCCGCGGCGCTCTCAATTAACGTGTTAAGACAAAACAAAAA 543

RESULT 6
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LOCUS A novel method of diagnosing, monitoring and staging lung cancer.
DEFINITION BD226775
ACCESSION BD226775.1 GI:33036545
VERSION JP 2002515262-A/6.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 543)
Yang,F., Macina,R.A. and Sun,Y.
A novel method of diagnosing, monitoring and staging lung cancer
Patent: JP 2002515262-A 6 28-MAY-2002;
DIADEXUS INC
OS Homo sapiens (human)
PN JP 2002515262-A/6
PD 28-MAY-2002 JP 2000549766
PR 12-MAY-1999 JP 2000549766
PR 21-MAY-1998 US 60/086212

PI FRI YANG, ROBERTO A MACINA, YONGMING SUN
PC C12N15/09, C12Q1/68, G01N33/50, C12N15/00
CC A novel method of diagnosing, monitoring and staging lung CC
FH Key Location/Qualifiers
FT source 1..543
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ORIGIN

Query Match 92.8%; Score 529; DB 6; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-79;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGGACCGGGTATTAAGAAAGCTCGTGGCTTGCCTCCGGGACGCGCAGATTCCCGCGC 60
DB 15 GCGAGGACCGGGTATTAAGAAAGCTCGTGGCTTGCCTCCGGGACGCGCAGATTCCCGCGC 74
QY 61 GCGCGAGCGCGGCGCATGAAGCTCGCGGCTCTGCGGAGCTGCGGCTGCTGCT 120
DB 75 GCGCGAGCGCGGCGCATGAAGCTCGCGGCTCTGCGGAGCTGCGGCTGCTGCT 134
QY 121 TGCAGCTCGGCTGCTCTTCTTAAAGTGGGCTCGGCAAGCTGTGGCCAGCCTGTGCT 180
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DB 255 AACCGCTGAAGCTCTGCTGAGCAGCTGGGATCCCGTGAACCACTCATAGAGGCG 314
QY 301 TCCAGAAAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGCGCTGAAGGCGCTGAAG 360
DB 315 TCCAGAAAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGCGCTGAAGGCGCTGAAG 374
QY 361 GCCCTGCTGGGGGCGCTGACAGTGTGGTGAAGCGGAGCGGAGCTGACATCACTGAG 420
DB 375 GCCCTGCTGGGGGCGCTGACAGTGTGGTGAAGCGGAGCGGAGCTGACATCACTGAG 434
QY 421 GACAAAGCGCTGCGCAACCGCGAGGCGTGAACCCCGCGGAGGAGGAGCGTCCATCC 480
DB 435 GACAAAGCGCTGCGCAACCGCGAGGCGTGAACCCCGCGGAGGAGGAGCGTCCATCC 494
QY 481 CTTTCCCGCGGCGCTCTCAATTAACGTGTTAAGACAAAACAAAAA 529
DB 495 CTTTCCCGCGGCGCTCTCAATTAACGTGTTAAGACAAAACAAAAA 543

RESULT 7
BD082142 519 bp DNA linear PAT 27-AUG-2002
LOCUS Reagents and methods useful for detecting diseases of the lung.
DEFINITION BD082142
ACCESSION BD082142.1 GI:22627752
VERSION JP 2001522225-A/6.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 519)
Medel,P.A.B., Cohen,M., Colpites,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodges,S.C., Klags,M.R., Kratochvil,J.D., Rapp,L.R.,
Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the lung
Patent: JP 2001522225-A 6 13-NOV-2001;

QY 1 GCGAGAACCGGGTATAGAAAGCCCTGCGGCTTCCCGGAGCCGAGGTTCCCGCGC 60
 Db 1 GCGAGAACCGGGTATAGAAAGCCCTGCGGCTTCCCGGAGCCGAGGTTCCCGCGC 60
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 Db 61 GCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTCTGGGCTCTGCGGAGCCCTGCGC 120
 QY 121 TGCAGCTCCGCTCTGCTTCTTAGGGCTCGGCCAAGCTGTGGCCCAAGCCTGTGCT 180
 Db 121 TGCAGCTCCGCTCTGCTTCTTAGGGCTCGGCCAAGCTGTGGCCCAAGCCTGTGCT 180
 QY 181 GCGCTGAGTCGCGCGAGGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGACCTTC 240
 Db 181 GCGCTGAGTCGCGCGAGGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGACCTTC 240
 QY 241 AACCCGCTGAAGCTCTGCTGAGCAGCTGTGGCATTCCTCGTGAACCACTCATAGAGGC 300
 Db 241 AACCCGCTGAAGCTCTGCTGAGCAGCTGTGGCATTCCTCGTGAACCACTCATAGAGGC 300
 QY 301 TCCGAGAAAGTGTGTGCTGAGCTGGATCCCAAGCCGCGGAGCCCTGAGAGCCCTGAG 360
 Db 301 TCCGAGAAAGTGTGTGCTGAGCTGGATCCCAAGCCGCGGAGCCCTGAGAGCCCTGAG 360
 QY 361 GCGCTGCGGGGCGCTTGAAGCTGTTGGCTGAGCCGAGCATCTACACTGAG 420
 Db 361 GCGCTGCGGGGCGCTTGAAGCTGTTGGCTGAGCCGAGCATCTACACTGAG 420
 QY 421 GACAAAGAGCTGCGCCAGCCGCGAGGGCTGAAAACCCGCGCGGAGAGACCTGCATCC 480
 Db 421 GACAAAGAGCTGCGCCAGCCGCGAGGGCTGAAAACCCGCGCGGAGAGACCTGCATCC 480
 QY 481 CCTTCCCCCGCCCTCTCAATTAACGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 540
 Db 481 CCTTCCCCCGCCCTCTCAATTAACGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 540
 QY 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570
 Db 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570

RESULT 4
 LOCUS AX201348 569 bp DNA linear PAT 30-AUG-2001
 DEFINITION Sequence 27 from Patent WO0153486.
 ACCESSION AX201348
 VERSION AX201348.1 GI:15391167
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Aghkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,
 Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,
 Stone, D.M., Watanabe, C.K., and Wood, W.I.
 TITLE Human signal peptide-containing protein
 JOURNAL Patent: WO 0153486-A 27 26-JUL-2001;
 Genentech, Inc. (US)

FEATURES
 source Location/Qualifiers
 1..569
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 99.8%; Score 569; DB 6; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1e-85;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGAACCGGGTATAGAAAGCCCTGCGGCTTCCCGGAGCCGAGGTTCCCGCGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 GCGAGAACCGGGTATAGAAAGCCCTGCGGCTTCCCGGAGCCGAGGTTCCCGCGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 GCGAGAACCGGGTATAGAAAGCCCTGCGGCTTCCCGGAGCCGAGGTTCCCGCGC 60
 QY 61 GCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTGCGGAGCTGCGGAGCCCTGCGC 120
 Db 61 GCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTCTGGGCTCTGCGGAGCCCTGCGC 120
 QY 121 TGCAGCTCCGCTCTGCTTCTTAGGGCTCGGCCAAGCTGTGGCCCAAGCCTGTGCT 180
 Db 121 TGCAGCTCCGCTCTGCTTCTTAGGGCTCGGCCAAGCTGTGGCCCAAGCCTGTGCT 180
 QY 181 GCGCTGAGTCGCGCGAGGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGACCTTC 240
 Db 181 GCGCTGAGTCGCGCGAGGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGACCTTC 240
 QY 241 AACCCGCTGAAGCTCTGCTGAGCAGCTGTGGCATTCCTCGTGAACCACTCATAGAGGC 300
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 Db 301 TCCGAGAAAGTGTGTGCTGAGCTGGATCCCAAGCCGCGGAGCCCTGAGAGCCCTGAG 360
 QY 361 GCGCTGCGGGGCGCTTGAAGCTGTTGGCTGAGCCGAGCATCTACACTGAG 420
 Db 361 GCGCTGCGGGGCGCTTGAAGCTGTTGGCTGAGCCGAGCATCTACACTGAG 420
 QY 421 GACAAAGAGCTGCGCCAGCCGCGAGGGCTGAAAACCCGCGCGGAGAGACCTGCATCC 480
 Db 421 GACAAAGAGCTGCGCCAGCCGCGAGGGCTGAAAACCCGCGCGGAGAGACCTGCATCC 480
 QY 481 CCTTCCCCCGCCCTCTCAATTAACGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 540
 Db 481 CCTTCCCCCGCCCTCTCAATTAACGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 540
 QY 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 569
 Db 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 569

RESULT 5
 LOCUS BD222719 543 bp DNA linear PAT 17-JUL-2003
 DEFINITION Human signal peptide-containing protein.
 ACCESSION BD222719
 VERSION BD222719.1 GI:33032489
 KEYWORDS JP 2002519030-A/65.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 543)
 AUTHORS Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,
 Baughn, M.R., Akredlom, I.E., Young, J.A., Yue, H., Patterson, C.,
 Reddy, R., Hillman, J.D., and Bandman, O.
 TITLE Human signal peptide-containing protein
 JOURNAL Patent: JP 2002519030-A 65 02-JUL-2002;
 INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)
 PN JP 2002519030-A/65
 PD 02-JUL-2002
 PR 25-JUN-1999 JP 2000557363
 PR 26-JUN-1998 US 60/090762, 31-JUL-1998 US 60/094983 PR
 01-OCT-1998 US 60/102686, 11-DEC-1998 US 60/112129 PI PREETI
 LAL, Y TOM TANG,GINA A GORGONE,NELI C CORLEY,KARL J PI GUEGLER,
 PI MARIAH R BAUGHN,INGRID E AKERBLDM,JANICE AU YOUNG,HENRY YUE,
 PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
 PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
 PC A61P25/00,
 PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
 C12N1/19,
 PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
 C12N15/00,
 PC A61K37/02,C12N5/00

COMMENT ABBOTT LABORATORIES
PN JP 2001522225-A/6
PD 13-NOV-2001
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/7917710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
PI N FRIEDMAN,
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
KLASS,
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
PI STROUPE
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1..519
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
ORIGIN
Query Match 91.1%; Score 519; DB 6; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.4e-77;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGAGAGACCGGGATATAGAAAGCTCGTGGCTTGGCCGAGCCGACAGTTTCCCGCGC 60
DB 1 GCGAGAGACCGGGATATAGAAAGCTCGTGGCTTGGCCGAGCCGACAGTTTCCCGCGC 60
QY 61 GCCCGAGACCCCGCGCATGAAGCTCGCGCCCTCTGGGGCTTGGCGGCTGTCTTC 120
DB 61 GCCCGAGACCCCGCGCATGAAGCTCGCGCCCTCTGGGGCTTGGCGGCTGTCTTC 120
QY 121 TCGAGCTCGCTCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCT 180
DB 121 TCGAGCTCGCTCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCT 180
QY 181 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGCGGAGCCTTGCCAAACCCCTCGGCACTTC 240
DB 181 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGCGGAGCCTTGCCAAACCCCTCGGCACTTC 240
QY 181 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGCGGAGCCTTGCCAAACCCCTCGGCACTTC 240
DB 181 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGCGGAGCCTTGCCAAACCCCTCGGCACTTC 240
QY 241 AACCCGCTGAAGTCTCTGCTGAGCAGCTGGGATCCCGGTGAACCACTCATAGAGGGC 300
DB 241 AACCCGCTGAAGTCTCTGCTGAGCAGCTGGGATCCCGGTGAACCACTCATAGAGGGC 300
QY 301 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 360
DB 301 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 360
QY 361 GCCCTGCTGGGGGCCCTTGACAGTGTGGCTGAGCGGAGACTGAGAGCATTTACACTGAG 420
DB 361 GCCCTGCTGGGGGCCCTTGACAGTGTGGCTGAGCGGAGACTGAGAGCATTTACACTGAG 420
QY 421 GACAAGACGCTGCCACCGCGGAGGGGCTGAAAAACCCCGCGGAGGAGAGCGGTTCATCC 480
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QY 481 CTTTCCCGCGCCCTCTCAATTAAGCTGTTAAGAGCA 519
DB 481 CTTTCCCGCGCCCTCTCAATTAAGCTGTTAAGAGCA 519
RESULT 8
BD082141
LOCUS BD082141 562 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082141
VERSION BD082141.1 GI:22627751
KEYWORDS JP 2001522225-A/5.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoidae; Andropogoneae; Zea.
AUTHORS 1 (bases 1 to 562)
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,
Russell, J.C. and Stroupe, S.D.
TITLE Reagents and methods useful for detecting diseases of the lung
JOURNAL Patient: JP 2001522225-A 5 13-NOV-2001;
ABBOTT LABORATORIES
COMMENT PN JP 2001522225-A/5
PD 13-NOV-2001
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/7917710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
TITLE JOURNAL
AUTHORS
ORIGIN
Query Match 91.0%; Score 518.6; DB 6; Length 562;
Best Local Similarity 99.8%; Pred. No. 2.8e-77;
Matches 518; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGAGAGACCGGGATATAGAAAGCTCGTGGCTTGGCCGAGCCGACAGTTTCCCGCGC 60
DB 44 GCGAGAGACCGGGATATAGAAAGCTCGTGGCTTGGCCGAGCCGACAGTTTCCCGCGC 103
QY 61 GCCCGAGACCCCGCGCATGAAGCTCGCGCCCTCTGGGGCTTGGCGGCTGTCTTC 120
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QY 121 TCGAGCTCGCTCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCT 180
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QY 164 TCGAGCTCGCTCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCT 223
DB 164 TCGAGCTCGCTCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCT 223
QY 181 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGGGAGCCTTGCCAAACCCCTCGGCACTTC 240
DB 224 GCGCTGAGAGTCGGCGGGGAGCGCGGGGCGGGAGCCTTGCCAAACCCCTCGGCACTTC 283
QY 241 AACCCGCTGAAGTCTCTGCTGAGCAGCTGGGATCCCGGTGAACCACTCATAGAGGGC 300
DB 284 AACCCGCTGAAGTCTCTGCTGAGCAGCTGGGATCCCGGTGAACCACTCATAGAGGGC 343
QY 301 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 360
DB 301 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 360
QY 344 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 403
DB 344 TCCCAAGAAGTGTGGCTGAGCTGGGTCCCAAGCGGTGGGGCCGTGAAGGCCCTGAAG 403
QY 361 GCCCTGCTGGGGGCCCTTGACAGTGTGGCTGAGCGGAGACTGAGAGCATTTACACTGAG 420
DB 404 GCCCTGCTGGGGGCCCTTGACAGTGTGGCTGAGCGGAGACTGAGAGCATTTACACTGAG 463
QY 421 GACAAGACGCTGCCACCGCGGAGGGCTGAAAAACCCCGCGGAGGAGAGCGGTTCATCC 480
DB 464 GACAAGACGCTGCCACCGCGGAGGGCTGAAAAACCCCGCGGAGGAGAGCGGTTCATCC 523
QY 481 CTTTCCCGCGCCCTCTCAATTAAGCTGTTAAGAGCA 519
DB 524 CTTTCCCGCGCCCTCTCAATTAAGCTGTTAAGAGCA 562

RESULT 9
LOCUS BC072673 530 bp mRNA linear PRI 25-JUN-2004
DEFINITION Homo sapiens secretoglobin, family 3A, member 1, mRNA (cDNA clone
MGC:87867 IMAGE:5753142), complete cds.
ACCESSION BC072673
VERSION BC072673.1 GI:49257439
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
Altehoefer S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,
Schaefer T.E., Brownstein M.J., Udell T.B., Toshiyuki S.,
Carinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.,
Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J.,
McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,
Wolter K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Faney J., Helton E., Kettman M., Madan A., Young A.C., Rodriguez S.,
Sanchez A., Whiting M., Madan A., Young A.C., Rodriguez S.,
Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D.,
Dickson M.C., Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E.,
Scherer A., Schein J.E., Jones S.J., and Marra M.A.
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
1477932
TITLE 2 (bases 1 to 530)
JOURNAL Strausberg R.
PUBMED Direct Submission
REFERENCE Submitted (07-JUN-2004) National Institutes of Health, Mammalian
AUTHORS Gene Collection (MGC), Cancer Genomics Office, National Cancer
TITLE Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
JOURNAL USA
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing By: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Aklter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooke, S.,
Districh, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripo, S., Thomas, P.J., Touchman, J.W.,
Tusberg, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
FEATURES
source Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LMUL at: <http://image.llnl.gov>
Series: IRK Plate: 174 Row: C Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 16418366.
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/mol_type="mRNA"
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Best Local Similarity 100.0%; Pred. No. 2,4e-76;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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22..336
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/db_xref="GI:49257440"
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1 CGCGCCCGAGAGCCCGGCGCATGAAGCTGCGCCCTCTCTGGAGCTCTGCGTGGCCCTG 117
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1 CGCGCCCGAGAGCCCGGCGCATGAAGCTGCGCCCTCTCTGGAGCTCTGCGTGGCCCTG 60
118 TCCTGCACTCTGCTGCTCTTCTTCTAGTGGAGCTGCGCCCAAGCTGTGGCCCAAGCTGTG 177
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181 CTGAACCCCTGTAAGCTCTGCTGAGCAAGCTGCGGCAATCCCGTGAACCACTCATTAAG 240
298 GCTGCGCTGAGTGTGAGGCGGAGGCGCGGCGCGGAGCCCTGCGGAGCCCTGCGGAG 357
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358 AAGGCGCTGCGGAGCCCTGCAAGTGTGCTGAGCGGAGCTGAGAGCATCTACACCT 417
301 AAGGCGCTGCGGAGCCCTGCAAGTGTGCTGAGCGGAGCTGAGAGCATCTACACCT 360
418 GAGGACAAAGACGCTGCCACCGGAGGAGGAGAAACCCCGCGGAGGAGACCGTCA 477
361 GAGGACAAAGACGCTGCCACCGGAGGAGGAGGAGAAACCCCGCGGAGGAGACCGTCA 420
478 TCCCGCTTCCCGCGCGCTGCTCAATTAAGCTGTGTTAAGCAAAAAA 537
421 TCCCGCTTCCCGCGCGCTGCTCAATTAAGCTGTGTTAAGCAAAAAA 480
538 AAAAAA 570
481 AAAAAA 513
RESULT 10
LOCUS BC029176
DEFINITION Homo sapiens secretoglobin, family 3A, member 1, mRNA (cDNA clone
MGC:34758 IMAGE:5180304), complete cds.
ACCESSION BC029176
VERSION BC029176.1 GI:20809672
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 503)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheaf C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scherz T.E., Brownstein M.J., Usdin T.B., Teshigahara S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 503)
Strausberg R.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsges, H., Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAK Plate: 50 Row: b Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OR analysis, Genomescan gene prediction.

FEATURES
source

1. 503
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/db_xref="taxon:9606"
/clone="MGC:34758 IMAGE:5180304"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_id="NIH MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. 503
/gene="SCGB3A1"
/note="synonyms: HIN-1, LUT105, UGRP2, HIN1, PnSP-2"
/db_xref="LocusID:92304"
/db_xref="MIM:606500"
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/gene="SCGB3A1"
/codon_start=1
/product="secretoglobin, family 3A, member 1"
/protein_id="AAH29176.1"

ORIGIN

Query Match 88.2%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 11e-74;
Matches 503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GTLAPLGLTNPILKLISLGI.PVNLHIGSQRCVAELPQVAVAKALKALGLTY
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QY 124 AGCTCGCTGCTGCTCTTTTAAAGTGGCTGGCCCAAGCTCTGCGGCTCTGCTGC 183
DB 61 AGCTCGCTGCTGCTCTTTTAAAGTGGCTGGCCCAAGCTCTGCGGCTCTGCTGC 120
QY 184 CTGGAAGCTCGGCGCGGAGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243
DB 121 CTGGAAGCTCGGCGCGGAGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 244 CCGCTGAAGCTCTGCTGAGACAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCC 303
DB 181 CCGCTGAAGCTCTGCTGAGACAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCC 240
QY 304 CAGAACTGTGTGGCTGAGCTGGGTCGCCAGCGCGTGGGCGCGTGAAGGCTCGAAGGCC 363
DB 241 CAGAACTGTGTGGCTGAGCTGGGTCGCCAGCGCGTGGGCGCGTGAAGGCTCGAAGGCC 300
QY 364 CTGCTGGGGGCGCTGAGCAATGTTGGCTGAGCGGCAATCTGAGCACTCACTGAGGAC 423
DB 301 CTGCTGGGGGCGCTGAGCAATGTTGGCTGAGCGGCAATCTGAGCACTCACTGAGGAC 360
QY 424 AAGACGCTGCCCAAGCGGCGGAGGCTGAAAACCGCGCGGAGGAGAGCGTCCATCCCT 483
DB 361 AAGACGCTGCCCAAGCGGCGGAGGCTGAAAACCGCGCGGAGGAGAGCGTCCATCCCT 420
QY 484 TCCCGCGGCGCTCTCAATTAACGTTGTTAAGAGCAAAAAAAAAAAAAAAAAAAAA 543
DB 421 TCCCGCGGCGCTCTCAATTAACGTTGTTAAGAGCAAAAAAAAAAAAAAAAAAAAA 480
QY 544 AAAAAAAAAAAAAAAAAAAAAA 566
DB 481 AAAAAAAAAAAAAAAAAAAAAA 503

RESULT 11
LOCUS HUMZB52D10 471 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone ZB52D10.
ACCESSION AF086152
VERSION AF086152.1 GI:3483497
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 471)
Woesener, J., Tan, F., Marra, M., Kueba, T., Yandell, M., Martin, J., Mart, G., Bowles, J., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chappell, J., Peterson, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behner, K., Hillier, L., Wilson, R. and Waterston, R.
Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 471)
AUTHORS Waterston, R.
TITLE Direct Submission

JOURNAL
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

FEATURES
The location of this clone is unknown.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:307219"
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Query Match 82.6%; Score 471; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.6e-69;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 CGGCCCCGAGCCCCCGCCCATGAAGCTCGCCGCTCTCGGAGCTCTGCGGCGCTG 117
DB 1 CGGCCCCGAGCCCCCGCCCATGAAGCTCGCCGCTCTCGGAGCTCTGCGGCGCTG 60
QY 118 TCTCGAGCTCCGCTGCTGCTTTCTTAAGTGGCTCGGCAAGCTGTGGCCAGCCTGTC 177
DB 61 TCTCGAGCTCCGCTGCTGCTTTCTTAAGTGGCTCGGCAAGCTGTGGCCAGCCTGTC 120
QY 178 GCTGCGTGAAGTGGCGCGCGAGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGAC 237
DB 121 GCTGCGTGAAGTGGCGCGCGAGCGCGGAGCCCTGCGCAACCCCTCGGAC 180
QY 238 CTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCACTCCCGTGAACCACTCATAGAG 297
DB 181 CTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCACTCCCGTGAACCACTCATAGAG 240
QY 298 GGCCTCCGAGAGTGTGTGCTGAGCTGGATCCCAAGCCGTGGGGCCGTGAAGGCGCTG 357
DB 241 GGCCTCCGAGAGTGTGTGCTGAGCTGGATCCCAAGCCGTGGGGCCGTGAAGGCGCTG 300
QY 358 AAGGCCCTGTGGGGGCGCTGAGCAGTGTGGTGGTGAAGCCGAGCATCTACACT 417
DB 301 AAGGCCCTGTGGGGGCGCTGAGCAGTGTGGTGGTGAAGCCGAGCATCTACACT 360
QY 418 GAGGACAAAGCGCTGCGCCACCGCGAGGGCTGAAAAACCCCGCGGGAGGAGACCTTCA 477
DB 361 GAGGACAAAGCGCTGCGCCACCGCGAGGGCTGAAAAACCCCGCGGGAGGAGACCTTCA 420
QY 478 TCCCTTTCCCGGCGCCCTCTCAATTAAGCGTTTAAGCAAAAAA 528
DB 421 TCCCTTTCCCGGCGCCCTCTCAATTAAGCGTTTAAGCAAAAAA 471

RESULT 12
AP436839 461 bp mRNA linear PRI 19-SEP-2003
LOCUS
DEFINITION Homo sapiens pneumo secretory protein 2 mRNA, complete cds.

ACCESSION
AF436839.1 GI:33315289

VERSION
Homo sapiens (human)

KEYWORDS
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 461)
Clippe, A., Iain, I. A., Lesouef, P. N., Bernard, A. and Knoops, B.
Molecular cloning of Pnsp-1, a protein of the respiratory tract with potential association to atopy

JOURNAL
TITLE
Unpublished
2 (bases 1 to 461)
Clippe, A., Bernard, A. and Knoops, B.
Direct Submission

REFERENCE
JOURNAL
Submitted (22-OCT-2001) Unit of Toxicology, Catholic University of Louvain, Clos Chapelle-aux-Champs, 30.54, Brussels, B 1200, Belgium

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="5"
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ORIGIN

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Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 CGGCCCCGAGCCCCCGCCCATGAAGCTCGCCGCTCTCGGAGCTCTGCGGCGCTG 117
DB 1 CGGCCCCGAGCCCCCGCCCATGAAGCTCGCCGCTCTCGGAGCTCTGCGGCGCTG 60
QY 118 TCTCGAGCTCCGCTGCTGCTTTCTTAAGTGGCTCGGCAAGCTGTGGCCAGCCTGTC 177
DB 61 TCTCGAGCTCCGCTGCTGCTTTCTTAAGTGGCTCGGCAAGCTGTGGCCAGCCTGTC 120
QY 178 GCTGCGTGAAGTGGCGCGAGCGCGGAGCCGCGGAGCCCTGCGCAACCCCTCGGAC 237
DB 121 GCTGCGTGAAGTGGCGCGAGCGCGGAGCCCTGCGCAACCCCTCGGAC 180
QY 238 CTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCACTCCCGTGAACCACTCATAGAG 297
DB 181 CTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCACTCCCGTGAACCACTCATAGAG 240
QY 298 GGCCTCCGAGAGTGTGTGCTGAGCTGGATCCCAAGCCGTGGGGCCGTGAAGGCGCTG 357
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QY 358 AAGGCCCTGTGGGGGCGCTGAGCAGTGTGGTGGTGAAGCCGAGCATCTACACT 417
DB 301 AAGGCCCTGTGGGGGCGCTGAGCAGTGTGGTGGTGAAGCCGAGCATCTACACT 360
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DB 361 GAGGACAAAGCGCTGCGCCACCGCGAGGGCTGAAAAACCCCGCGGGAGGAGACCTTCA 420
QY 478 TCCCTTTCCCGGCGCCCTCTCAATTAAGCGTTTAAGAGC 518
DB 421 TCCCTTTCCCGGCGCCCTCTCAATTAAGCGTTTAAGAGC 461

RESULT 13

CQ776781 461 bp DNA linear PAT 11-MAR-2004
LOCUS CQ776781 Sequence 467 from Patent EP1394274.
DEFINITION CQ776781
ACCESSION CQ776781
VERSION CQ776781.1 GI:45380171
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhara, K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 467 03-MAR-2004;
Genex Research, Inc. (JP)
FEATURES
source 1..461
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Query Match 80.3%; Score 457.8; DB 6; Length 461;
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Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 178 GCTGCGCTGAGTGGCGGCGGAGGCGGCGGCGGAGCCCTGCGCAACCCCTCGGCAAC 237
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QY 238 CTCACCCCGCTGAAGCTCTGCTGAGAGCTGAGGCACTCCCGTGAACCACTCATAGAG 297
DB 181 CTCACCCCGCTGAAGCTCTGCTGAGAGCTGAGGCACTCCCGTGAACCACTCATAGAG 240
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DB 421 TCCCTTTCCCGGCGCCCTCTCAATAAAGTGTGAAGAC 461
RESULT 14
AY040564 461 bp mRNA linear PRI 15-AUG-2001
LOCUS AY040564 Homo sapiens HIN-1 putative cytokine mRNA, complete cds.
DEFINITION AY040564
ACCESSION AY040564
VERSION AY040564.1 GI:15079187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Krop, I.E., Sgroi, D., Porter, D.A., Lunetta, K.L., LeVangie, R.,

Seth, P., Kaelin, C.M., Rhee, E., Rosenberg, M., Schmitt, S.,
Marks, J.R., Pagon, Z., Belina, D., Razumovic, J., and Polyak, K.
HIN-1, a putative cytokine highly expressed in normal but not
cancerous mammary epithelial cells
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9796-9801 (2001)
JOURNAL 21396515
MEDLINE 11481438
PUBMED 11481438
REFERENCE 2 (bases 1 to 461)
AUTHORS Polyak, K., Krop, I. and Sgroi, D.
TITLE Direct Submission
JOURNAL Submitted (15-JUN-2001) Adult Oncology, Dana-Farber Cancer
Institute, 44 Binney St. D740C, Boston, MA 02115, USA
FEATURES
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FG"
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Query Match 80.3%; Score 457.8; DB 9; Length 461;
Best Local Similarity 99.6%; Pred. No. 4.3e-67;
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 58 CCGGCCCCGAGACCCCGGCGCATGAAGCTGCGCCCTCTCTGGGCGCTGCGTGGCCCTG 117
DB 1 CCGGCCCCGAGACCCCGGCGCATGAAGCTGCGCCCTCTCTGGGCGCTGCGTGGCCCTG 60
QY 118 TCCTGAGCTCCGCTGCTGCTTCTTAAGTGGGCTCGGCCCAAGCTGAGCCCAAGCTGTC 177
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DB 301 AAGGCCCTGAGGAGCCCTGAGCAGTGTGCTGAGCCGAGACTGAGCATCTACACT 360
QY 418 GAGGACAAAGCGTGGCCACCCGCGAGAGGCTGAAAAACCCCGCGGAGAGACGCTCA 477
DB 361 GAGGACAAAGCGTGGCCACCCGCGAGAGGCTGAAAAACCCCGCGGAGAGACGCTCA 420
QY 478 TCCCTTTCCCGGCGCCCTCTCAATAAAGTGTGAAGAC 518
DB 421 TCCCTTTCCCGGCGCCCTCTCAATAAAGTGTGAAGAC 461
RESULT 15
AF313458 347 bp mRNA linear PRI 19-NOV-2002
LOCUS AF313458 Homo sapiens UGRP2 mRNA, complete cds.
DEFINITION AF313458
ACCESSION AF313458
VERSION AF313458.1 GI:16565421

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE 1 (bases 1 to 347)
Nimi,T., Keck-Waggoner,C.L., Popescu,N.C., Zhou,Y., Levitt,R.C.
and Kimura,S.
UGRP1, a uteroglobin/Clara cell secretory protein-related protein,
is a novel lung-enriched downstream target gene for the
T/EBP/NKX2.1 homeodomain transcription factor
Mol. Endocrinol. 15 (11), 2021-2036 (2001)
JOURNAL MEDLINE 21539178
PUBMED 11682631
REFERENCE 2 (bases 1 to 347)
AUTHORS Nimi,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A., Srisodasai,A.,
Zimonjic,D.B., Keck-Waggoner,C.L., Popescu,N.C. and Kimura,S.
Cloning, expression, and chromosomal localization of the mouse gene
(Scgb3a1, alias Ugrp2) that encodes a member of the novel
uteroglobin-related protein gene family
Cytogenet. Genome Res. 97 (1-2), 120-127 (2002)
JOURNAL 12438750
PUBMED 12438750
REFERENCE 3 (bases 1 to 347)
AUTHORS Nimi,T. and Kimura,S.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2000) Laboratory of Metabolism, National Cancer
Institute, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN

Query Match 60.6%; Score 345.4; DB 9; Length 347;
Best Local Similarity 99.7%; Pred. No. 2.9e-48;
Matches 346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 69 CCCCCCGCCATGAAGCTGCGCGCCCTCTGCGGAGCTGTGCTGAGCCCTGTCTGCGAGCTC 128
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QY 129 CGCTGCTGCTTTCTTAGTGAGGCTGGGCCAAGCTGTGGCCAGCTGTGCTGCGCTGGA 188
Db 61 CGCTGCTGCTTTCTTAGTGAGGCTGGGCCAAGCTGTGGCCAGCTGTGCTGCGCTGGA 120
QY 189 GTCCGCGCGGAGGCGCGGAGCCGAGACCTCTGGCCAAACCCCTCGGACCCCTCAACCCGCT 248
Db 121 GTCCGCGCGGAGGCGCGGAGCCGAGACCTCTGGCCAAACCCCTCGGACCCCTCAACCCGCT 180
QY 249 GAAGCTCCTGTAGAGAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAA 308
Db 181 GAAGCTCCTGTAGAGAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAA 240
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Db 241 GTGTGTGTGCTGAGCTGGTCCCGAGGCGGTGGGGGCGGTGAAGGCGCTGAAAGCCCTGCT 300
QY 369 GGGGGCCCTGAGAGGTTTGGCTGAGCCGAGACTGAGACATCTACAC 415
Db 301 GGGGGCCCTGAGAGGTTTGGCTGAGCCGAGACTGAGACATCTACAC 347

Search completed: March 8, 2005, 07:46:36
Job time : 2729 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 03:05:46 ; Search time 3119 Seconds
(without alignments)
6956.279 Million cell updates/sec

Title: US-09-989-731-407

Perfect score: 570

Sequence: 1 gcgagcagccgggtataagaa.....aaaaaaaaaaaaaaaaaaaaa 570

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	485	85.1	496	4	BI818715 603037535
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4	478.4	83.9	880	4	BI489765 603032283
5	472	82.8	473	5	BM920793 AGENCOURT
6	470.4	82.5	473	5	BM920794 AGENCOURT
7	467.4	82.0	496	4	BI819795 603041303
8	462.4	81.1	1059	5	BQ067622 AGENCOURT
9	461	80.9	1083	5	BM921624 AGENCOURT
10	457.6	80.3	550	2	AM974727 EST386817
11	456.4	80.1	491	4	BI819014 603031130
12	452.6	80.0	680	4	BI812791 603035866
13	452.6	79.4	961	4	BI819045 603031186
14	450.6	79.1	885	4	BI824102 603039244
15	448	78.6	472	5	BM977779 UI-CF-EN1
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17	428	75.1	437	6	CB049699 NISC_gj12
18	425	74.6	425	1	AI187341 603037400
19	424	74.4	424	1	AI187340 603037400
20	420.8	73.8	424	1	AI174409 603037400
21	418.4	73.4	420	1	AI193619 603032441
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23	413	72.5	413	1	AI174557 603032441
24	412.8	72.4	416	2	BF221778 7062602.x

25	411.2	72.1	526	1	AA742697
26	410.6	72.0	1004	4	BI769722
27	407.4	71.5	662	5	BM982112
28	407.4	71.5	711	5	BM982925
29	407.4	71.5	718	6	CA313307
30	407.4	71.5	731	5	BM980649
31	405	71.1	878	4	BI823159
32	394.6	69.2	1000	4	BI908998
33	387.8	68.0	476	4	BI818534
34	383.4	67.3	407	4	BI820788
35	378	66.3	378	1	AI684641
36	377.8	66.3	416	4	BI490604
37	366.4	64.3	435	6	CB049698 NISC_gj12
38	344.2	60.4	887	4	BI818788
39	339.8	59.6	343	1	AA649864
40	320	56.1	320	5	BU679439
41	306.6	53.8	335	1	AA902200
42	293.4	51.5	380	7	N95182
43	285.4	50.1	323	2	BE707758
44	280	49.1	389	7	W72786
45	277.8	48.7	427	7	W76414
46	275	48.2	424	7	W7934
47	240	42.1	248	5	BU607563
48	218	38.2	218	1	AI972960
49	207	36.3	207	1	AI686647
50	201.4	35.3	203	2	AM173160
51	193	33.9	204	5	BM286746
52	186	32.6	186	5	BQ270088
53	170.8	30.0	668	5	BM975405
54	169.8	29.8	620	5	BQ045452
55	166	29.1	166	7	CK825885
56	151.8	26.6	464	1	AI858018
57	147.4	25.9	295	2	BF848524
58	126.8	22.2	142	8	AZ576152
59	123.4	21.6	551	6	CA787079
60	118.4	20.8	467	5	BX511579
61	118.4	20.8	467	5	CA460315
62	117.8	20.7	484	7	CF108592
63	117.4	20.6	389	1	AI390146
64	114.4	20.1	1089	6	CA459759
65	110.2	19.3	400	7	W08303
66	110	19.3	402	7	W20910
67	109.8	19.3	350	5	BY119477
68	109.8	19.0	1059	6	CA461596
69	108.2	18.8	340	5	BY117555
70	107.4	18.3	495	3	AK003988
71	104.4	17.4	400	1	AI011836
72	99.2	16.8	325	5	BY119621
73	96	16.4	463	6	BY704236
74	93.2	16.4	421	1	AI413570
75	83.2	14.6	221	1	BI768092
76	79.2	13.9	760	4	BI768092
77	78.2	13.7	448	9	CG548614
78	78.2	13.7	976	4	BI518636
79	77.4	13.6	302	5	BY119435
80	75.8	13.3	363	2	BE030469
81	74.8	13.1	999	4	BM416251
82	73.4	12.9	910	2	BF034716
83	73.2	12.8	333	7	CO887707
84	73.2	12.8	807	2	BE964961
85	73.2	12.8	998	4	BM415943
86	72.8	12.8	1101	2	BE899528
87	72.6	12.7	666	4	BE757952
88	72.2	12.7	132	4	BG91831
89	72.2	12.7	278	1	AI491798
90	72.2	12.7	903	2	BE965527
91	72	12.6	508	5	BM968150
92	71.8	12.6	545	7	CF331737
93	71.6	12.6	1251	9	AG290040
94	71.4	12.5	188	2	BF814578
95	71.4	12.5	975	4	BM415718
96	71.2	12.5	947	5	BO651674
97	71.2	12.5	1002	4	BM415588

C 98	71.2	12.5	1178	4	BM415062	BM415062	OP20132 M	C 171	68	11.9	884	8	BH162006
C 99	71	12.5	200	1	A1400725	A1400725	CP93H12.X	C 172	68	11.9	925	9	CNS0091P
C 100	71	12.5	664	7	CO872324	CO872324	Bovgen.00	C 173	68	11.9	939	7	BM415961
C 101	71	12.5	910	4	BM416476	BM416476	OP21571 M	C 174	68	11.9	1003	2	BE949662
C 102	71	12.5	1205	4	BR899377	BR899377	601681306	C 175	67.8	11.9	212	2	BF814409
C 103	70.8	12.4	940	9	CNS03Q04	CNS03Q04	Tetradon	C 176	67.8	11.9	321	1	A1050881
C 104	70.6	12.4	358	2	BE033190	BE033190	MA	C 177	67.8	11.9	487	5	BM941152
C 105	70.6	12.4	387	2	AM074161	AM074161	XSO8F05.X	C 178	67.8	11.9	857	7	CN330658
C 106	70.6	12.4	990	4	BM416248	BM416248	OP21336 M	C 179	67.8	11.9	1031	4	BM415361
C 107	70.4	12.4	1020	4	BM416248	BM416248	OP20479 M	C 180	67.6	11.9	191	1	A1680457
C 108	70.4	12.4	1146	5	BH186923	BH186923	BOVGEN.16	C 181	67.6	11.9	273	6	CD108810
C 109	70.2	12.3	500	7	CO887700	CO887700	Bovgen.16	C 182	67.6	11.9	328	1	A1866503
C 110	70	12.3	825	2	BR863159	BR863159	BOVGEN.16	C 183	67.6	11.9	337	7	CF315071
C 111	70	12.3	919	4	BM415717	BM415717	OP20797 M	C 184	67.6	11.9	406	2	AM051727
C 112	69.8	12.2	152	6	CB455595	CB455595	712748 MA	C 185	67.6	11.9	460	5	BO933742
C 113	69.8	12.2	188	4	B1015384	B1015384	MR4-ET024	C 186	67.6	11.9	600	7	CF177299
C 114	69.8	12.2	248	7	CO887695	CO887695	Bovgen.16	C 187	67.6	11.9	716	7	CF181809
C 115	69.6	12.2	188	4	BG991080	BG991080	MR2-HT118	C 188	67.6	11.9	901	9	CNS0760F
C 116	69.6	12.2	656	6	CD752026	CD752026	AGENCOURT	C 189	67.6	11.9	938	4	BM415706
C 117	69.6	12.2	656	6	CD752026	CD752026	AGENCOURT	C 190	67.6	11.9	1083	5	BO673308
C 118	69.6	12.2	971	4	BM415133	BM415133	OP20211 M	C 191	67.4	11.8	171	4	BG956194
C 119	69.6	12.2	973	4	BM415133	BM415133	OP20265 M	C 192	67.4	11.8	235	7	CN160387
C 120	69.6	12.2	989	4	BM416249	BM416249	OP21337 M	C 193	67.4	11.8	238	7	CN266177
C 121	69.4	12.2	161	7	CO872278	CO872278	Bovgen.00	C 194	67.4	11.8	256	5	BO601072
C 122	69.4	12.2	240	1	AJ461053	AJ461053	MA	C 195	67.4	11.8	323	1	BM415082
C 123	69.4	12.2	349	2	BE235962	BE235962	143605 MA	C 196	67.4	11.8	358	2	BF452643
C 124	69.4	12.2	359	2	BE235961	BE235961	MA	C 197	67.4	11.8	393	6	CD805897
C 125	69.4	12.2	815	2	BE235961	BE235961	601659543	C 198	67.4	11.8	401	2	BE851065
C 126	69.4	12.2	925	9	CNS0091P	CNS0091P	AL053013 Drosoph11	C 199	67.4	11.8	454	7	CK429028
C 127	69.4	12.2	927	7	CV068663	CV068663	f2 new ch	C 200	67.4	11.8	404	7	CF327700
C 128	69.2	12.1	311	2	BR210200	BR210200	MA	C 201	67.4	11.8	532	7	CO872951
C 129	69.2	12.1	535	2	CF328267	CF328267	MA	C 202	67.4	11.8	532	1	A1627201
C 130	69	12.1	169	2	BF815196	BF815196	MA	C 203	67.4	11.8	592	1	AL675201
C 131	69	12.1	654	7	CF328267	CF328267	MA	C 204	67.4	11.8	788	2	BE390669
C 132	69	12.1	873	7	CF328267	CF328267	MA	C 205	67.4	11.8	787	7	CK147989
C 133	69	12.1	1012	2	BE364959	BE364959	601658736	C 206	67.4	11.8	885	2	BE536377
C 134	69	12.1	1591	2	CK452644	CK452644	908296 MA	C 207	67.4	11.8	938	4	BM416545
C 135	68.8	12.1	591	2	BE364959	BE364959	601658736	C 208	67.4	11.8	1402	4	B1490155
C 136	68.8	12.1	595	2	AM161812	AM161812	MA	C 209	67.2	11.8	2041	3	BC033500
C 137	68.8	12.1	969	5	BO957033	BO957033	AGENCOURT	C 210	67.2	11.8	233	1	A1801556
C 138	68.8	12.1	1215	2	BE612450	BE612450	602333203	C 211	67.2	11.8	304	2	CN315267
C 139	68.8	12.1	1215	2	BE612450	BE612450	602333203	C 212	67.2	11.8	314	5	BUI95249
C 140	68.6	12.0	209	4	B1019329	B1019329	MR3-MT032	C 213	67.2	11.8	343	5	CF584272
C 141	68.6	12.0	872	4	BM415957	BM415957	OP21039 M	C 214	67.2	11.8	358	1	BM416545
C 142	68.6	12.0	932	7	CNS02813	CNS02813	AGENCOURT	C 215	67.2	11.8	358	5	BK486581
C 143	68.6	12.0	1042	7	BM416154	BM416154	OP21241 M	C 216	67.2	11.8	358	5	BK486581
C 144	68.6	12.0	1817	3	BC041022	BC041022	Homo. sarp1	C 217	67.2	11.8	358	5	BK486581
C 145	68.4	12.0	157	4	BG988354	BG988354	MR3-HT120	C 218	67.2	11.8	358	5	BK486581
C 146	68.4	12.0	184	1	A1263331	A1263331	q987901.x	C 219	67.2	11.8	358	5	BK486581
C 147	68.4	12.0	190	4	B1023122	B1023122	MR3-MT032	C 220	67.2	11.8	358	5	BK486581
C 148	68.4	12.0	195	2	AM193872	AM193872	xm19A03.x	C 221	67.2	11.8	358	5	BK486581
C 149	68.4	12.0	272	2	AM192375	AM192375	x182G06.x	C 222	67.2	11.8	358	5	BK486581
C 150	68.4	12.0	542	4	BI491427	BI491427	f08F12.W	C 223	67.2	11.8	358	5	BK486581
C 151	68.4	12.0	597	7	CN317153	CN317153	AGENCOURT	C 224	67.2	11.8	358	5	BK486581
C 152	68.4	12.0	903	4	BG178352	BG178352	602330117	C 225	67.2	11.8	358	5	BK486581
C 153	68.4	12.0	917	4	BM416465	BM416465	OP21560 M	C 226	67.2	11.8	358	5	BK486581
C 154	68.4	12.0	950	4	BM415041	BM415041	OP20110 M	C 227	67.2	11.8	358	5	BK486581
C 155	68.4	12.0	1453	3	BC039034	BC039034	Homo. sarp1	C 228	67.2	11.8	358	5	BK486581
C 156	68.2	12.0	1463	2	BG680287	BG680287	602629179	C 229	67.2	11.8	358	5	BK486581
C 157	68.2	12.0	261	1	BF814525	BF814525	MR2-CI018	C 230	66.8	11.7	193	6	CB974556
C 158	68.2	12.0	261	1	BF814525	BF814525	MR2-CI018	C 231	66.8	11.7	193	6	CB974556
C 159	68.2	12.0	724	4	BG108334	BG108334	602280341	C 232	66.8	11.7	196	4	B1002369
C 160	68.2	12.0	724	4	BG108334	BG108334	602280341	C 233	66.8	11.7	386	1	A1696956
C 161	68.2	12.0	1443	4	BG757031	BG757031	602710448	C 234	66.8	11.7	458	7	CO896144
C 162	68.2	12.0	1631	2	BE743507	BE743507	601573394	C 235	66.8	11.7	531	7	CF314165
C 163	68	11.9	139	2	BF812963	BF812963	MR2-CI018	C 236	66.8	11.7	562	7	CF881520
C 164	68	11.9	203	1	BF812963	BF812963	MR2-CI018	C 237	66.8	11.7	743	2	BE964597
C 165	68	11.9	214	4	BG993819	BG993819	MR3-HT127	C 238	66.8	11.7	817	2	BE964597
C 166	68	11.9	231	1	A1561299	A1561299	tq24H04.x	C 239	66.8	11.7	836	4	CO873183
C 167	68	11.9	232	1	A1783530	A1783530	t236E11.x	C 240	66.8	11.7	858	4	BI416515
C 168	68	11.9	375	1	A1631057	A1631057	t232A06.x	C 241	66.8	11.7	911	4	BM416484
C 169	68	11.9	377	1	A1632036	A1632036	t232A06.x	C 242	66.8	11.7	964	4	BE612862
C 170	68	11.9	508	6	CH523675	CH523675	UI-M-GK0-	C 243	66.8	11.7	1199	5	BM903573

536	64.6	11.3	461	6	CB844257	M15E--5213	C 609	64.2	11.3	420	1	AJ485582
C 537	64.6	11.3	467	6	CB052899	NISC_g110	C 610	64.2	11.3	431	4	CF333677
C 538	64.6	11.3	468	4	BI492374	dfc3rd03.w	C 611	64.2	11.3	441	7	BG574118
539	64.6	11.3	473	4	BM553962		C 612	64.2	11.3	445	7	CK998611
540	64.6	11.3	506	7	CK484235		C 613	64.2	11.3	448	6	CD239708
541	64.6	11.3	516	7	CN783044	a1_F001.4	C 614	64.2	11.3	453	7	CO881716
542	64.6	11.3	523	4	BM281946	k123c05.y	C 615	64.2	11.3	460	5	BQ387565
C 543	64.6	11.3	614	8	BM166902	ENTRO90TR	C 616	64.2	11.3	472	6	CB343321
544	64.6	11.3	824	4	BM415861	OP0943.M	C 617	64.2	11.3	476	9	CN502R01
545	64.6	11.3	824	7	CF784510		C 618	64.2	11.3	484	5	BQ395565
546	64.6	11.3	857	5	BU954681		C 619	64.2	11.3	500	3	CR640278
C 547	64.6	11.3	877	2	BE964755	601658407	C 620	64.2	11.3	503	7	CO874516
C 548	64.6	11.3	910	7	CV069478	WPAExh15	C 621	64.2	11.3	515	6	CO804196
C 549	64.6	11.3	940	6	BE963809	601657460	C 622	64.2	11.3	526	6	CD678874
550	64.6	11.3	1016	5	BO718364	AGENCOURT	C 623	64.2	11.3	526	7	CK776971
551	64.6	11.3	1615	9	AG311072	Mus_muscu	C 624	64.2	11.3	544	6	CB053489
C 552	64.4	11.3	179	4	BG168185	602341586	C 625	64.2	11.3	550	5	BP372967
C 553	64.4	11.3	241	1	AJ653346	AJ653346	C 626	64.2	11.3	553	1	AJ683714
554	64.4	11.3	250	7	CK407161	AUF_ILfvr	C 627	64.2	11.3	566	7	CF319654
555	64.4	11.3	253	6	CB048443		C 628	64.2	11.3	572	5	BP306440
556	64.4	11.3	263	6	CB048444	NISC_g104	C 629	64.2	11.3	585	1	AJ539847
C 557	64.4	11.3	278	6	CB052708		C 630	64.2	11.3	588	1	AJ952114
558	64.4	11.3	288	6	BE754450	207961.MA	C 631	64.2	11.3	604	7	CO877670
C 559	64.4	11.3	305	2	AM007309	wf54h02.x	C 632	64.2	11.3	608	5	BQ397388
C 560	64.4	11.3	337	2	AM151970	xf71a07.x	C 633	64.2	11.3	627	7	CF314054
C 561	64.4	11.3	349	6	CD723632	0124f02.y	C 634	64.2	11.3	637	7	CF549772
C 562	64.4	11.3	367	1	AI857760	w121g04.x	C 635	64.2	11.3	745	7	CO872976
563	64.4	11.3	398	3	AF116644	Homo_sapi	C 636	64.2	11.3	750	2	BE886858
C 564	64.4	11.3	435	7	CF320474	HD--11-G0	C 637	64.2	11.3	792	7	CO960760
565	64.4	11.3	439	5	BQ802093	WHE2822.A	C 638	64.2	11.3	846	2	BE963818
566	64.4	11.3	441	2	AM953817	ESPT66007	C 639	64.2	11.3	882	4	BG828051
C 567	64.4	11.3	523	7	CF316038		C 640	64.2	11.3	897	4	BF983626
568	64.4	11.3	789	5	BU414617	603667993	C 641	64.2	11.3	924	8	BM415316
C 569	64.4	11.3	848	4	BG474227	602561846	C 642	64.2	11.3	932	8	AZ542647
570	64.4	11.3	879	2	BE969452	601649669	C 643	64.2	11.3	934	4	BM415897
C 571	64.4	11.3	932	2	BE965022	601658805	C 644	64.2	11.3	937	7	CF581299
C 572	64.4	11.3	1077	5	BM907650	AGENCOURT	C 645	64.2	11.3	944	2	BE536909
C 573	64.4	11.3	1165	4	BG488803	602534774	C 646	64.2	11.3	949	7	CF581465
C 574	64.4	11.3	1206	4	BM009429	603628937	C 647	64.2	11.3	986	7	CF581387
C 575	64.4	11.3	1271	2	BE964600	601658526	C 648	64.2	11.3	989	7	CV069665
576	64.4	11.3	2129	3	BC033579	Homo_sapi	C 649	64.2	11.3	1014	2	BE965471
C 577	64.2	11.3	112	4	BI001345		C 650	64.2	11.3	1023	2	BE964045
C 578	64.2	11.3	137	2	BF811802		C 651	64.2	11.3	1227	7	CF579397
C 579	64.2	11.3	155	4	BI015381	MR4-ET024	C 652	64.2	11.3	1246	5	BO433823
C 580	64.2	11.3	179	2	BF921092	MR2-NT013	C 653	64.2	11.3	1258	4	BM394234
C 581	64.2	11.3	183	4	AI587121	cf53e03.x	C 654	64.2	11.3	1844	3	BE962888
C 582	64.2	11.3	233	1	BG956916	OVO-CY073	C 655	64.2	11.3	3168	3	HSM808894
583	64.2	11.3	257	2	AM656503	108790.MA	C 656	64.2	11.3	3169	3	HSM808852
584	64.2	11.3	259	4	BI539149	451338.MA	C 657	64.2	11.3	318	4	BG996119
C 585	64.2	11.3	272	1	AJ799419		C 658	64.2	11.3	318	4	BG996119
C 586	64.2	11.3	277	1	AI952360	wx72902.x	C 659	64.2	11.3	318	4	BG996119
C 587	64.2	11.3	279	1	AI863411	cf240h07.x	C 660	64.2	11.3	318	4	BG996119
C 588	64.2	11.3	313	1	AI624668	cf43c0d6.x	C 661	64.2	11.3	318	4	BG996119
C 589	64.2	11.3	313	1	AI824444	cf70c010.x	C 662	64.2	11.3	318	4	BG996119
C 590	64.2	11.3	318	6	CA501316	MHE4032.B	C 663	64.2	11.3	318	4	BG996119
C 591	64.2	11.3	330	1	AI285732	qUB1d02.x	C 664	64.2	11.3	318	4	BG996119
C 592	64.2	11.3	332	7	CF328738		C 665	64.2	11.3	318	4	BG996119
C 593	64.2	11.3	335	7	CN840208		C 666	64.2	11.3	318	4	BG996119
C 594	64.2	11.3	336	7	CF317484	HD--07-D0	C 667	64.2	11.3	318	4	BG996119
C 595	64.2	11.3	338	7	CF330404	NACL--06-	C 668	64.2	11.3	318	4	BG996119
596	64.2	11.3	343	4	BM445435	1111d1.1	C 669	64.2	11.3	318	4	BG996119
C 597	64.2	11.3	345	1	AI682837	w669a01.x	C 670	64.2	11.3	318	4	BG996119
598	64.2	11.3	347	5	BU679066	UT-CF-DU1	C 671	64.2	11.3	318	4	BG996119
C 599	64.2	11.3	349	1	AI339388	qf02a12.x	C 672	64.2	11.3	318	4	BG996119
C 600	64.2	11.3	353	6	CB050372	NISC_gj16	C 673	64.2	11.3	318	4	BG996119
601	64.2	11.3	356	5	BM925639	AGENCOURT	C 674	64.2	11.3	318	4	BG996119
C 602	64.2	11.3	369	2	AM168296	xg62907.x	C 675	64.2	11.3	318	4	BG996119
603	64.2	11.3	386	4	BI898861	480651.MA	C 676	64.2	11.3	318	4	BG996119
C 604	64.2	11.3	391	2	AI887221	wm37d11.x	C 677	64.2	11.3	318	4	BG996119
C 605	64.2	11.3	394	2	AM090494	xc84b11.x	C 678	64.2	11.3	318	4	BG996119
606	64.2	11.3	394	6	CD105470	AGENCOURT	C 679	64.2	11.3	318	4	BG996119
C 607	64.2	11.3	412	2	AM130584	xf54c09.x	C 680	64.2	11.3	318	4	BG996119
608	64.2	11.3	413	7	CK467628	938943.MA	C 681	64.2	11.3	318	4	BG996119

C 682	64	11.2	374	7	CF310089	CF310089 ABF--04-J	C 755	63.8	11.2	608	1	AA485953
C 683	64	11.2	389	7	CO891668	CO891668 BoyGen.19	C 756	63.8	11.2	641	1	AA648546
C 684	64	11.2	391	2	AM084812	AM084812 xc63d08.x	C 757	63.8	11.2	642	1	BI858668
C 685	64	11.2	403	5	BO524385	BO524385 NISC no04	C 758	63.8	11.2	686	6	CD108918
C 686	64	11.2	424	1	AA790256	AA790256 yw16D09.f	C 759	63.8	11.2	721	7	CN165144
C 687	64	11.2	438	6	CD672592	CD672592 f9j3h05.x	C 760	63.8	11.2	840	2	BE965071
C 688	64	11.2	439	7	CO876707	CO876707 BoyGen.05	C 761	63.8	11.2	939	7	CV068729
C 689	64	11.2	454	5	BO397624	BO397624 NISC_rg28	C 762	63.8	11.2	952	7	CK403655
C 690	64	11.2	464	7	CF332023	CF332023 NACL--08-	C 763	63.8	11.2	956	2	BE964759
C 691	64	11.2	469	5	BO525723	BO525723 NISC no12	C 764	63.8	11.2	1003	4	BI258565
C 692	64	11.2	476	7	CF313501	CF313501 ABF--08-E	C 765	63.8	11.2	1005	4	BM416485
C 693	64	11.2	489	5	BU704582	BU704582 UT-M-PP0	C 766	63.8	11.2	1034	2	BE966775
C 694	64	11.2	495	7	CF122597	CF122597 UT-HR-CH0	C 767	63.8	11.2	1090	2	BE966775
C 695	64	11.2	500	6	CB285207	CB285207 CMDID_F06	C 768	63.8	11.2	1280	2	BE966570
C 696	64	11.2	514	5	BE013956	BE013956 125497 MA	C 769	63.8	11.2	1282	4	BE966570
C 697	64	11.2	515	6	CB716451	CB716451 AMGNNUC.S	C 770	63.8	11.2	1801	2	BE734492
C 698	64	11.2	538	1	AL727686	AL727686 AL727686	C 771	63.8	11.2	1801	2	BE734492
C 700	64	11.2	545	5	BO527470	BO527470 NISC no22	C 772	63.6	11.2	127	7	CF321991
C 701	64	11.2	564	7	CF313743	CF313743 HD--01.P1	C 773	63.6	11.2	143	5	BU534646
C 702	64	11.2	564	7	AJ746726	AJ746726 L0525C01-	C 774	63.6	11.2	164	2	AM129271
C 703	64	11.2	575	1	BM123450	BM123450 NISC_g107	C 775	63.6	11.2	167	1	AI251830
C 704	64	11.2	575	1	BM123450	BM123450 NISC_mq09	C 776	63.6	11.2	171	4	BI001715
C 705	64	11.2	596	6	BO389769	BO389769 NISC_mq09	C 777	63.6	11.2	175	4	BI001534
C 706	64	11.2	646	7	CF175945	CF175945 799960 MA	C 778	63.6	11.2	180	1	AI445990
C 707	64	11.2	738	2	BE974632	BE974632 601680655	C 779	63.6	11.2	180	1	AI445990
C 708	64	11.2	752	7	CO876882	CO876882 BoyGen.05	C 780	63.6	11.2	193	5	BM536365
C 709	64	11.2	754	1	AV176495	AV176495 AV176495	C 781	63.6	11.2	200	1	AI467537
C 710	64	11.2	760	1	AV176495	AV176495 AV176495	C 782	63.6	11.2	204	1	AI467537
C 711	64	11.2	814	9	CNS02171	CNS02171	C 783	63.6	11.2	210	2	AM438793
C 712	64	11.2	825	2	BE884441	BE884441 601510725	C 784	63.6	11.2	210	2	CR557393
C 713	64	11.2	825	2	BE884441	BE884441 601510725	C 785	63.6	11.2	210	2	CR557393
C 714	64	11.2	921	4	BE965731	BE965731 601510725	C 786	63.6	11.2	219	7	BU844285
C 715	64	11.2	921	4	BE965731	BE965731 601510725	C 787	63.6	11.2	222	5	BU844285
C 716	64	11.2	939	2	BE965731	BE965731 601510725	C 788	63.6	11.2	231	5	BU844285
C 717	64	11.2	949	9	CF508232	CF508232 SATL.793	C 789	63.6	11.2	242	7	CF329593
C 718	64	11.2	965	2	BE733429	BE733429 601645847	C 790	63.6	11.2	248	2	AM131331
C 719	64	11.2	1006	3	BC020164	BC020164 Homo.88p1	C 791	63.6	11.2	264	4	BU768996
C 720	64	11.2	1033	4	BE287631	BE287631 602384454	C 792	63.6	11.2	269	1	AI446046
C 721	64	11.2	1066	4	BE287631	BE287631 602384454	C 793	63.6	11.2	270	1	AI446046
C 722	64	11.2	1110	3	BE964792	BE964792 601658445	C 794	63.6	11.2	275	1	AI446046
C 723	64	11.2	1501	3	BC048715	BC048715 Nts muscu	C 795	63.6	11.2	275	1	AI446046
C 724	63.8	11.2	185	1	AA145131	AA145131 Nts muscu	C 796	63.6	11.2	285	1	AI446046
C 725	63.8	11.2	185	1	AA145131	AA145131 Nts muscu	C 797	63.6	11.2	285	1	AI446046
C 726	63.8	11.2	237	8	AZ576306	AZ576306 AST-2T006	C 798	63.6	11.2	297	2	AM168320
C 727	63.8	11.2	239	1	AZ576306	AZ576306 AST-2T006	C 799	63.6	11.2	298	6	CD678431
C 728	63.8	11.2	258	1	AI890833	AI890833 wmb1f09.x	C 800	63.6	11.2	301	2	AM586772
C 729	63.8	11.2	267	4	BM055713	BM055713 t937509.x	C 801	63.6	11.2	302	6	AM586772
C 730	63.8	11.2	271	1	AI335203	AI335203 t937509.x	C 802	63.6	11.2	302	6	AM586772
C 731	63.8	11.2	305	2	BE753670	BE753670 t937509.x	C 803	63.6	11.2	306	1	AI589261
C 732	63.8	11.2	305	2	BE753670	BE753670 t937509.x	C 804	63.6	11.2	306	1	AI589261
C 733	63.8	11.2	308	6	CA391724	CA391724 EST12499	C 805	63.6	11.2	330	6	CD734235
C 734	63.8	11.2	310	2	BE753670	BE753670 t937509.x	C 806	63.6	11.2	333	6	CD734235
C 735	63.8	11.2	344	1	BE753670	BE753670 t937509.x	C 807	63.6	11.2	347	7	CF334388
C 736	63.8	11.2	346	1	BE753670	BE753670 t937509.x	C 808	63.6	11.2	348	7	CF334388
C 737	63.8	11.2	355	2	AM102942	AM102942 t937509.x	C 809	63.6	11.2	354	5	BE965071
C 738	63.8	11.2	355	2	AM102942	AM102942 t937509.x	C 810	63.6	11.2	361	5	BE965071
C 739	63.8	11.2	368	7	CF980718	CF980718 t937509.x	C 811	63.6	11.2	361	5	BE965071
C 740	63.8	11.2	383	1	CF980718	CF980718 t937509.x	C 812	63.6	11.2	363	7	BM124294
C 741	63.8	11.2	386	7	CF980718	CF980718 t937509.x	C 813	63.6	11.2	363	7	BM124294
C 742	63.8	11.2	394	1	AA831987	AA831987 t937509.x	C 814	63.6	11.2	365	2	AM908388
C 743	63.8	11.2	402	1	AA831987	AA831987 t937509.x	C 815	63.6	11.2	369	6	CD693970
C 744	63.8	11.2	419	7	AL698015	AL698015 t937509.x	C 816	63.6	11.2	373	2	BE767496
C 745	63.8	11.2	430	2	AM102924	AM102924 t937509.x	C 817	63.6	11.2	375	1	AI089851
C 746	63.8	11.2	432	2	AM102924	AM102924 t937509.x	C 818	63.6	11.2	376	1	AI089851
C 747	63.8	11.2	451	7	CF298500	CF298500 t937509.x	C 819	63.6	11.2	382	6	CD223536
C 748	63.8	11.2	451	7	CF298500	CF298500 t937509.x	C 820	63.6	11.2	382	6	CD223536
C 749	63.8	11.2	459	6	CB451927	CB451927 t937509.x	C 821	63.6	11.2	399	2	BE440117
C 750	63.8	11.2	490	6	CB451927	CB451927 t937509.x	C 822	63.6	11.2	399	2	BE440117
C 751	63.8	11.2	497	7	CK451805	CK451805 t937509.x	C 823	63.6	11.2	401	6	CA337608
C 752	63.8	11.2	526	7	CK451805	CK451805 t937509.x	C 824	63.6	11.2	401	7	CF337825
C 753	63.8	11.2	535	6	CB217910	CB217910 NISC_md05	C 825	63.6	11.2	404	5	BM923886
C 754	63.8	11.2	587	4	BM923886	BM923886 t937509.x	C 826	63.6	11.2	404	5	BM923886
							C 827	63.6	11.2	405	5	BM923886

C 828	63.6	11.2	406	5	B0526114	B0526114 NISC no14	901	63.6	11.2	772	1	AV758339	AV758339
C 829	63.6	11.2	411	1	AI811845	AI811845 tW45C12.x	902	63.6	11.2	777	6	CB985960	CB985960
830	63.6	11.2	412	1	AL597750	AL597750 DKF20313B	903	63.6	11.2	784	1	AI541048	AI541048
831	63.6	11.2	413	5	BP368161	BP368161 BP368161	904	63.6	11.2	790	5	BU957936	BU957936
832	63.6	11.2	413	5	BP368309	BP368309 BP368309	905	63.6	11.2	797	1	AV757205	AV757205
833	63.6	11.2	414	1	AV681639	AV681639 AV681639	906	63.6	11.2	816	6	CB310550	CB310550
C 834	63.6	11.2	414	6	CB217992	CB217992 NISC -0084	C 907	63.6	11.2	818	8	AZ538703	AZ538703
835	63.6	11.2	414	6	CB839976	CB839976 M15E-0084	C 908	63.6	11.2	822	2	BF204483	BF204483
836	63.6	11.2	423	7	CK652119	CK652119 LP22103.5	909	63.6	11.2	832	7	CK128668	CK128668
837	63.6	11.2	427	5	B0564291	B0564291 AGENCOURT	910	63.6	11.2	833	5	BU564378	BU564378
838	63.6	11.2	428	7	CR753607	CR753607 DKF2p469F	911	63.6	11.2	843	4	BG109959	BG109959
839	63.6	11.2	429	6	CD238001	CD238001 FNPASE10	912	63.6	11.2	846	1	AV757362	AV757362
840	63.6	11.2	431	6	CD106183	CD106183 AGENCOURT	913	63.6	11.2	847	4	BI759832	BI759832
841	63.6	11.2	434	7	CR629072	CR629072 DKF2p4681	914	63.6	11.2	856	4	BI524056	BI524056
842	63.6	11.2	435	7	CR832270	CR832270 AGENCOURT	915	63.6	11.2	870	5	BU958052	BU958052
843	63.6	11.2	436	6	CD175136	CD175136 AGENCOURT	C 916	63.6	11.2	897	8	BH162937	BH162937
844	63.6	11.2	441	4	BI761192	BI761192 603043418	917	63.6	11.2	900	4	BI255205	BI255205
845	63.6	11.2	444	6	CD173669	CD173669 AGENCOURT	918	63.6	11.2	901	5	BU181433	BU181433
846	63.6	11.2	445	5	BY393726	BY393726 BY393726	919	63.6	11.2	905	4	BG575878	BG575878
847	63.6	11.2	446	6	CD238662	CD238662 FNPBD07	C 920	63.6	11.2	913	4	BM416526	BM416526
848	63.6	11.2	449	6	CD239598	CD239598 FNPBD09	C 921	63.6	11.2	917	2	BE964089	BE964089
849	63.6	11.2	449	6	CD239647	CD239647 FNPBDH10	C 922	63.6	11.2	919	5	BU533717	BU533717
850	63.6	11.2	450	5	BP327554	BP327554 BP327554	923	63.6	11.2	930	6	CD389750	CD389750
851	63.6	11.2	450	6	CD239723	CD239723 FNPBXG09	924	63.6	11.2	932	6	CNS0070E	CNS0070E
C 852	63.6	11.2	455	5	BU587776	BU587776 AGENCOURT	925	63.6	11.2	932	9	CD5050735	CD5050735
853	63.6	11.2	456	6	CD386558	CD386558 AGENCOURT	926	63.6	11.2	933	6	CD388765	CD388765
854	63.6	11.2	457	6	CD386558	CD386558 AGENCOURT	C 927	63.6	11.2	938	6	CD5050219	CD5050219
855	63.6	11.2	458	4	BG108189	BG108189 602280058	C 928	63.6	11.2	940	4	BM415207	BM415207
856	63.6	11.2	460	5	BP367883	BP367883 BP367883	929	63.6	11.2	940	6	CD386618	CD386618
857	63.6	11.2	464	7	CN842303	CN842303 AGENCOURT	930	63.6	11.2	941	5	BU540230	BU540230
858	63.6	11.2	471	7	CK349199	CK349199 hcg7fha10A	931	63.6	11.2	948	6	CD390144	CD390144
859	63.6	11.2	472	5	B0627411	B0627411 rc7f9g03.Y	932	63.6	11.2	949	6	CD387866	CD387866
860	63.6	11.2	473	6	CA337220	CA337220 NISC_Lv10	933	63.6	11.2	950	6	CD389726	CD389726
861	63.6	11.2	473	6	CD640969	CD640969 AGENCOURT	934	63.6	11.2	951	6	CD386657	CD386657
C 862	63.6	11.2	476	2	AM080357	AM080357 xes52e10.x	935	63.6	11.2	951	6	CD389712	CD389712
863	63.6	11.2	482	7	CK128725	CK128725 AGENCOURT	936	63.6	11.2	962	6	CD386074	CD386074
864	63.6	11.2	483	6	CD639284	CD639284 AGENCOURT	937	63.6	11.2	963	6	CD387343	CD387343
865	63.6	11.2	486	5	BQ526855	BQ526855 NISC no18	C 938	63.6	11.2	965	5	BQ276670	BQ276670
866	63.6	11.2	486	5	BQ526855	BQ526855 NISC no18	C 939	63.6	11.2	965	5	BU503863	BU503863
867	63.6	11.2	492	4	BG574039	BG574039 602595887	940	63.6	11.2	971	6	CD385074	CD385074
C 868	63.6	11.2	492	5	BO232971	BO232971 NISC no02	941	63.6	11.2	978	6	CD051220	CD051220
869	63.6	11.2	497	5	BQ523971	BQ523971 NISC no02	942	63.6	11.2	978	6	CD388087	CD388087
870	63.6	11.2	513	1	AV756451	AV756451 AV756451	943	63.6	11.2	980	6	CD243153	CD243153
871	63.6	11.2	518	1	AV756566	AV756566 t197903.x	944	63.6	11.2	988	6	CB193687	CB193687
C 872	63.6	11.2	526	1	A1476086	A1476086 t197903.x	945	63.6	11.2	988	6	CD246455	CD246455
873	63.6	11.2	543	5	BQ395278	BQ395278 NISC ng14	946	63.6	11.2	988	6	CD579612	CD579612
874	63.6	11.2	550	5	BM919518	BM919518 AGENCOURT	947	63.6	11.2	992	6	CD050633	CD050633
C 875	63.6	11.2	555	5	BK550071	BK550071 BK550071	948	63.6	11.2	997	6	CD050261	CD050261
876	63.6	11.2	582	5	BP367580	BP367580 BP367580	C 949	63.6	11.2	1003	2	BE967251	BE967251
877	63.6	11.2	582	2	BE256257	BE256257 601117687	C 950	63.6	11.2	1003	2	BM415018	BM415018
878	63.6	11.2	589	1	AV714347	AV714347 AV714347	951	63.6	11.2	1010	5	BQ233647	BQ233647
879	63.6	11.2	602	1	AV734425	AV734425 AV734425	952	63.6	11.2	1016	6	CD049879	CD049879
880	63.6	11.2	603	1	AV732976	AV732976 AV732976	953	63.6	11.2	1020	6	CD050745	CD050745
881	63.6	11.2	605	1	AV714341	AV714341 AV714341	C 954	63.6	11.2	1032	2	BE965997	BE965997
C 882	63.6	11.2	612	2	BE964260	BE964260 601657952	955	63.6	11.2	1041	6	CD389041	CD389041
883	63.6	11.2	626	1	A1696829	A1696829 w674601.x	956	63.6	11.2	1043	6	CD249756	CD249756
884	63.6	11.2	624	6	CD771403	CD771403 AGENCOURT	957	63.6	11.2	1056	6	CD385652	CD385652
C 885	63.6	11.2	628	7	CO877522	CO877522 BoveGen_05	C 958	63.6	11.2	1065	5	BM907561	BM907561
C 886	63.6	11.2	632	4	BG169501	BG169501 602321313	959	63.6	11.2	1083	3	CD243051	CD243051
887	63.6	11.2	654	2	BF682593	BF682593 602117218	C 960	63.6	11.2	1084	7	CK230695	CK230695
C 888	63.6	11.2	660	1	A1256022	A1256022 u176f04.x	961	63.6	11.2	1088	4	CD048594	CD048594
C 889	63.6	11.2	670	2	AM166977	AM166977 xg69c11.x	962	63.6	11.2	1100	4	BG108233	BG108233
890	63.6	11.2	684	6	CD237052	CD237052 FNPAGB05	963	63.6	11.2	1111	2	BE286899	BE286899
891	63.6	11.2	685	1	AV733869	AV733869 AV733869	964	63.6	11.2	1117	4	BM460752	BM460752
C 892	63.6	11.2	702	5	BU803007	BU803007 SJFPAQ09	C 965	63.6	11.2	1156	5	BQ688321	BQ688321
893	63.6	11.2	707	1	AV681884	AV681884 AV681884	966	63.6	11.2	1158	6	CD389915	CD389915
894	63.6	11.2	709	6	CD639498	CD639498 AGENCOURT	967	63.6	11.2	1200	5	BM920102	BM920102
895	63.6	11.2	716	4	BG113863	BG113863 602284313	C 968	63.6	11.2	1307	7	CO390224	CO390224
896	63.6	11.2	726	6	CD638566	CD638566 AGENCOURT	C 969	63.6	11.2	1349	4	BG120046	BG120046
897	63.6	11.2	736	6	CD638562	CD638562 AGENCOURT	C 970	63.6	11.2	1349	4	BI490160	BI490160
898	63.6	11.2	737	6	AV758146	AV758146 AV758146	C 971	63.6	11.2	1446	4	BI490258	BI490258
899	63.6	11.2	741	1	AV760340	AV760340 AV760340	C 972	63.6	11.2	1603	3	BF983779	BF983779
900	63.6	11.2	748	1	AV757984	AV757984 AV757984	C 973	63.6	11.2	2146	3	BC027965	BC027965

C 974	63.4	11.1	168	7	CF307645	ABF--01-C	C1047	63.2	11.1	185	4	BG977864
C 975	63.4	11.1	176	4	BI001620		1048	63.2	11.1	186	6	CD522269
C 976	63.4	11.1	189	5	BQ636470		1049	63.2	11.1	206	7	CD522269
C 977	63.4	11.1	189	7	CK622931	hdi0a12.y	1049	63.2	11.1	206	7	CK454091
C 978	63.4	11.1	191	5	BK951840	BM190413	1050	63.2	11.1	212	1	AA904121
C 979	63.4	11.1	201	4	BM190413	BM190413	1051	63.2	11.1	216	1	AA904121
C 980	63.4	11.1	204	5	BK491289	BM190413	1052	63.2	11.1	220	4	BG956197
C 981	63.4	11.1	205	4	BK491289	BM190413	1053	63.2	11.1	221	4	BG956197
C 982	63.4	11.1	216	7	CF313061	hdi0a12.y	1054	63.2	11.1	231	2	AA426349
C 983	63.4	11.1	215	7	CF313061	hdi0a12.y	1055	63.2	11.1	231	2	AA426349
C 984	63.4	11.1	242	5	BK630001	hdi0a12.y	1056	63.2	11.1	232	2	AA426349
C 985	63.4	11.1	256	4	BI001686	MR3-CN014	1057	63.2	11.1	232	2	AA426349
C 986	63.4	11.1	269	4	BG980699	MR3-CN014	1058	63.2	11.1	241	4	BI490962
C 987	63.4	11.1	272	4	BG980699	MR3-CN014	1059	63.2	11.1	242	6	CA376650
C 988	63.4	11.1	294	6	CF322658	hdi0a12.y	1060	63.2	11.1	250	1	AI590943
C 989	63.4	11.1	317	1	AI628292	hdi0a12.y	1061	63.2	11.1	253	1	AI590943
C 990	63.4	11.1	324	4	BM117156	hdi0a12.y	1062	63.2	11.1	257	1	AI590943
C 991	63.4	11.1	347	6	CF322658	hdi0a12.y	1063	63.2	11.1	259	6	CD32647
C 992	63.4	11.1	352	2	AM183621	hdi0a12.y	1064	63.2	11.1	268	4	BI056598
C 993	63.4	11.1	364	4	BI047951	hdi0a12.y	1065	63.2	11.1	270	1	AI922216
C 994	63.4	11.1	367	7	CF298661	hdi0a12.y	1066	63.2	11.1	282	6	CA24357
C 995	63.4	11.1	385	7	CF318493	hdi0a12.y	1067	63.2	11.1	284	1	AI679758
C 996	63.4	11.1	389	7	CF318493	hdi0a12.y	1068	63.2	11.1	296	2	BE683816
C 997	63.4	11.1	390	2	BE904691	hdi0a12.y	1069	63.2	11.1	302	2	BE683816
C 998	63.4	11.1	402	1	AI610822	hdi0a12.y	1070	63.2	11.1	305	7	BE683816
C 999	63.4	11.1	402	1	AI610822	hdi0a12.y	1071	63.2	11.1	305	7	BE683816
C 1000	63.4	11.1	418	6	CD672135	hdi0a12.y	1072	63.2	11.1	305	7	BE683816
C 1001	63.4	11.1	423	6	CD672135	hdi0a12.y	1073	63.2	11.1	305	7	BE683816
C 1002	63.4	11.1	445	2	BF499456	hdi0a12.y	1074	63.2	11.1	313	6	CR052707
C 1003	63.4	11.1	451	2	BF499456	hdi0a12.y	1075	63.2	11.1	313	6	CR052707
C 1004	63.4	11.1	451	1	AI590781	hdi0a12.y	1076	63.2	11.1	313	7	CF457299
C 1005	63.4	11.1	453	1	AI627896	hdi0a12.y	1077	63.2	11.1	314	1	AI680280
C 1006	63.4	11.1	489	1	AI747892	hdi0a12.y	1078	63.2	11.1	328	1	AI250848
C 1007	63.4	11.1	490	1	AI747892	hdi0a12.y	1079	63.2	11.1	328	1	AI250848
C 1008	63.4	11.1	513	6	CD371875	hdi0a12.y	1080	63.2	11.1	343	4	BG061653
C 1009	63.4	11.1	525	4	BI081066	hdi0a12.y	1081	63.2	11.1	343	7	CO091671
C 1010	63.4	11.1	547	3	CR733851	hdi0a12.y	1082	63.2	11.1	344	7	CO091671
C 1011	63.4	11.1	565	7	CR733851	hdi0a12.y	1083	63.2	11.1	357	1	AI818977
C 1012	63.4	11.1	569	3	CR733851	hdi0a12.y	1084	63.2	11.1	357	1	AI818977
C 1013	63.4	11.1	595	5	BP42823	hdi0a12.y	1085	63.2	11.1	380	1	AI818977
C 1014	63.4	11.1	599	5	BP42823	hdi0a12.y	1086	63.2	11.1	380	2	AM104125
C 1015	63.4	11.1	620	1	AI953803	hdi0a12.y	1087	63.2	11.1	388	4	BM541202
C 1016	63.4	11.1	622	1	AI953803	hdi0a12.y	1088	63.2	11.1	396	6	BI538821
C 1017	63.4	11.1	666	6	CD639267	hdi0a12.y	1089	63.2	11.1	405	1	AI872051
C 1018	63.4	11.1	716	2	BE964295	hdi0a12.y	1090	63.2	11.1	407	2	BE964295
C 1019	63.4	11.1	808	5	AG044147	hdi0a12.y	1091	63.2	11.1	424	4	BI002625
C 1020	63.4	11.1	834	5	BU938828	hdi0a12.y	1092	63.2	11.1	424	4	BI002625
C 1021	63.4	11.1	849	7	BU938828	hdi0a12.y	1093	63.2	11.1	426	6	CD521867
C 1022	63.4	11.1	853	1	AI613492	hdi0a12.y	1094	63.2	11.1	438	2	AM117907
C 1023	63.4	11.1	854	5	BU938828	hdi0a12.y	1095	63.2	11.1	447	2	BE668722
C 1024	63.4	11.1	871	2	BE964295	hdi0a12.y	1096	63.2	11.1	449	6	CD238993
C 1025	63.4	11.1	880	6	CA484582	hdi0a12.y	1097	63.2	11.1	449	6	CD238993
C 1026	63.4	11.1	880	6	CA484582	hdi0a12.y	1098	63.2	11.1	451	6	CD238993
C 1027	63.4	11.1	915	4	BM415846	hdi0a12.y	1099	63.2	11.1	461	6	CD238993
C 1028	63.4	11.1	933	4	BM415846	hdi0a12.y	1100	63.2	11.1	471	1	AI920950
C 1029	63.4	11.1	959	5	BU153873	hdi0a12.y	1101	63.2	11.1	471	1	AI920950
C 1030	63.4	11.1	979	2	BE964420	hdi0a12.y	1102	63.2	11.1	477	6	CD520910
C 1031	63.4	11.1	1020	2	BE964420	hdi0a12.y	1103	63.2	11.1	489	6	CD520910
C 1032	63.4	11.1	1059	7	CK162692	hdi0a12.y	1104	63.2	11.1	490	6	CD520910
C 1033	63.4	11.1	1288	4	BG105187	hdi0a12.y	1105	63.2	11.1	501	2	AM411324
C 1034	63.4	11.1	1450	4	BG297378	hdi0a12.y	1106	63.2	11.1	511	4	BG044288
C 1035	63.4	11.1	1450	4	BG297378	hdi0a12.y	1107	63.2	11.1	521	7	CO871780
C 1036	63.2	11.1	112	4	BG956245	hdi0a12.y	1108	63.2	11.1	558	5	BO388769
C 1037	63.2	11.1	140	7	CR451113	hdi0a12.y	1109	63.2	11.1	558	7	BO388769
C 1038	63.2	11.1	144	6	CR451113	hdi0a12.y	1110	63.2	11.1	569	7	BO388769
C 1039	63.2	11.1	159	4	BG996109	hdi0a12.y	1111	63.2	11.1	571	5	BO390342
C 1040	63.2	11.1	162	5	BK500485	hdi0a12.y	1112	63.2	11.1	589	2	AM263588
C 1041	63.2	11.1	165	1	AI890806	hdi0a12.y	1113	63.2	11.1	595	1	AV726624
C 1042	63.2	11.1	174	4	BG980736	hdi0a12.y	1114	63.2	11.1	610	7	CO875303
C 1043	63.2	11.1	175	6	CD520960	hdi0a12.y	1115	63.2	11.1	613	6	CA325681
C 1044	63.2	11.1	180	2	AM193134	hdi0a12.y	1116	63.2	11.1	650	6	CA325681
C 1045	63.2	11.1	181	4	BI001545	hdi0a12.y	1117	63.2	11.1	655	1	AV705341
C 1046	63.2	11.1	181	4	BI001545	hdi0a12.y	1118	63.2	11.1	655	1	AV705341

1266	62.8	11.0	263	4	BG894579	355249	MA	1339	62.8	11.0	1266	5	BO433927	BO433927	AGENCY
1267	62.8	11.0	270	1	AI446605	412506	x	1340	62.8	11.0	1352	2	BE735370	BE735370	AGENCY
1268	62.8	11.0	271	4	BI539105	451270	MA	1341	62.8	11.0	1456	2	BI490278	BI490278	AGENCY
1269	62.8	11.0	301	6	CA825339	R57C06	lv	1342	62.8	11.0	2042	3	HSM03181	HSM03181	AGENCY
1270	62.8	11.0	284	4	BMS72662	FX56A06	y	1343	62.8	11.0	3233	3	HSM03971	HSM03971	AGENCY
1271	62.8	11.0	316	4	BI073294	K29B12	y	1344	62.8	11.0	120	4	BI775433	BI775433	AGENCY
1272	62.8	11.0	316	7	AI642173	UC46G05	x	1345	62.8	11.0	133	4	BI042301	BI042301	AGENCY
1273	62.8	11.0	317	1	AI642173	UC46G05	x	1346	62.8	11.0	160	4	BI042301	BI042301	AGENCY
1274	62.8	11.0	322	7	CO876326	FX56A06	y	1347	62.8	11.0	167	7	CF968987	CF968987	AGENCY
1275	62.8	11.0	339	1	AI872159	FX56A06	y	1348	62.8	11.0	179	4	BE987113	BE987113	AGENCY
1276	62.8	11.0	339	1	AI872159	FX56A06	y	1349	62.8	11.0	182	2	BE061389	BE061389	AGENCY
1277	62.8	11.0	339	1	AI872159	FX56A06	y	1350	62.8	11.0	186	1	AI918449	AI918449	AGENCY
1278	62.8	11.0	339	1	AI872159	FX56A06	y	1351	62.8	11.0	187	7	AI863191	AI863191	AGENCY
1279	62.8	11.0	339	1	AI872159	FX56A06	y	1352	62.8	11.0	187	7	CF202153	CF202153	AGENCY
1280	62.8	11.0	339	1	AI872159	FX56A06	y	1353	62.8	11.0	194	7	CF354681	CF354681	AGENCY
1281	62.8	11.0	339	1	AI872159	FX56A06	y	1354	62.8	11.0	209	1	CA336685	CA336685	AGENCY
1282	62.8	11.0	339	1	AI872159	FX56A06	y	1355	62.8	11.0	210	7	AI919107	AI919107	AGENCY
1283	62.8	11.0	339	1	AI872159	FX56A06	y	1356	62.8	11.0	211	7	CF301886	CF301886	AGENCY
1284	62.8	11.0	339	1	AI872159	FX56A06	y	1357	62.8	11.0	212	1	AI804983	AI804983	AGENCY
1285	62.8	11.0	339	1	AI872159	FX56A06	y	1358	62.8	11.0	237	1	AI653923	AI653923	AGENCY
1286	62.8	11.0	339	1	AI872159	FX56A06	y	1359	62.8	11.0	240	1	AI477067	AI477067	AGENCY
1287	62.8	11.0	339	1	AI872159	FX56A06	y	1360	62.8	11.0	254	4	BE980504	BE980504	AGENCY
1288	62.8	11.0	339	1	AI872159	FX56A06	y	1361	62.8	11.0	254	7	CF316185	CF316185	AGENCY
1289	62.8	11.0	339	1	AI872159	FX56A06	y	1362	62.8	11.0	258	1	AI302559	AI302559	AGENCY
1290	62.8	11.0	339	1	AI872159	FX56A06	y	1363	62.8	11.0	263	7	CO880166	CO880166	AGENCY
1291	62.8	11.0	339	1	AI872159	FX56A06	y	1364	62.8	11.0	268	4	BM534724	BM534724	AGENCY
1292	62.8	11.0	339	1	AI872159	FX56A06	y	1365	62.8	11.0	273	1	AI256528	AI256528	AGENCY
1293	62.8	11.0	339	1	AI872159	FX56A06	y	1366	62.8	11.0	277	7	TI8682	TI8682	AGENCY
1294	62.8	11.0	339	1	AI872159	FX56A06	y	1367	62.8	11.0	278	4	BE991089	BE991089	AGENCY
1295	62.8	11.0	339	1	AI872159	FX56A06	y	1368	62.8	11.0	289	1	AI455046	AI455046	AGENCY
1296	62.8	11.0	339	1	AI872159	FX56A06	y	1369	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1297	62.8	11.0	339	1	AI872159	FX56A06	y	1370	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1298	62.8	11.0	339	1	AI872159	FX56A06	y	1371	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1299	62.8	11.0	339	1	AI872159	FX56A06	y	1372	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1300	62.8	11.0	339	1	AI872159	FX56A06	y	1373	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1301	62.8	11.0	339	1	AI872159	FX56A06	y	1374	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1302	62.8	11.0	339	1	AI872159	FX56A06	y	1375	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1303	62.8	11.0	339	1	AI872159	FX56A06	y	1376	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1304	62.8	11.0	339	1	AI872159	FX56A06	y	1377	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1305	62.8	11.0	339	1	AI872159	FX56A06	y	1378	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1306	62.8	11.0	339	1	AI872159	FX56A06	y	1379	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1307	62.8	11.0	339	1	AI872159	FX56A06	y	1380	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1308	62.8	11.0	339	1	AI872159	FX56A06	y	1381	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1309	62.8	11.0	339	1	AI872159	FX56A06	y	1382	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1310	62.8	11.0	339	1	AI872159	FX56A06	y	1383	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1311	62.8	11.0	339	1	AI872159	FX56A06	y	1384	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1312	62.8	11.0	339	1	AI872159	FX56A06	y	1385	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1313	62.8	11.0	339	1	AI872159	FX56A06	y	1386	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1314	62.8	11.0	339	1	AI872159	FX56A06	y	1387	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1315	62.8	11.0	339	1	AI872159	FX56A06	y	1388	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1316	62.8	11.0	339	1	AI872159	FX56A06	y	1389	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1317	62.8	11.0	339	1	AI872159	FX56A06	y	1390	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1318	62.8	11.0	339	1	AI872159	FX56A06	y	1391	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1319	62.8	11.0	339	1	AI872159	FX56A06	y	1392	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1320	62.8	11.0	339	1	AI872159	FX56A06	y	1393	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1321	62.8	11.0	339	1	AI872159	FX56A06	y	1394	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1322	62.8	11.0	339	1	AI872159	FX56A06	y	1395	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1323	62.8	11.0	339	1	AI872159	FX56A06	y	1396	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1324	62.8	11.0	339	1	AI872159	FX56A06	y	1397	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1325	62.8	11.0	339	1	AI872159	FX56A06	y	1398	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1326	62.8	11.0	339	1	AI872159	FX56A06	y	1399	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1327	62.8	11.0	339	1	AI872159	FX56A06	y	1400	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1328	62.8	11.0	339	1	AI872159	FX56A06	y	1401	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1329	62.8	11.0	339	1	AI872159	FX56A06	y	1402	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1330	62.8	11.0	339	1	AI872159	FX56A06	y	1403	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1331	62.8	11.0	339	1	AI872159	FX56A06	y	1404	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1332	62.8	11.0	339	1	AI872159	FX56A06	y	1405	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1333	62.8	11.0	339	1	AI872159	FX56A06	y	1406	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1334	62.8	11.0	339	1	AI872159	FX56A06	y	1407	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1335	62.8	11.0	339	1	AI872159	FX56A06	y	1408	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1336	62.8	11.0	339	1	AI872159	FX56A06	y	1409	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1337	62.8	11.0	339	1	AI872159	FX56A06	y	1410	62.8	11.0	291	1	AI476527	AI476527	AGENCY
1338	62.8	11.0	339	1	AI872159	FX56A06	y	1411	62.8	11.0	291	1	AI476527	AI476527	AGENCY

c1412	62.6	11.0	447	7	CF330760	CF330760	NACLT--06-
c1413	62.6	11.0	448	7	CF320118	HD--10-N2	
c1414	62.6	11.0	449	7	CO876345	BOVgen 04	
1415	62.6	11.0	452	1	AA242021	nm22b05.r	
c1416	62.6	11.0	456	6	CB075621	h249c07.D	
c1417	62.6	11.0	458	7	CF122636	UI-HF-CH0	
c1418	62.6	11.0	455	7	CF309960	ABR--04-F	
1419	62.6	11.0	473	5	BU589899	AGENCOURT	
1420	62.6	11.0	477	2	BF074766	BR074766	222302.MA
c1421	62.6	11.0	479	5	BQ394664	NISC-ng10	
1422	62.6	11.0	479	7	CO873730	BOVgen_02	
1423	62.6	11.0	483	5	BX744466	BX744466	
c1424	62.6	11.0	489	5	BQ388879	NISC_mq04	
c1425	62.6	11.0	492	5	BO520185	NISC_n103	
c1426	62.6	11.0	496	5	BX567561	BX567561	
c1427	62.6	11.0	504	7	CF330727	NACLT--06-	
c1428	62.6	11.0	508	1	AI805144	td11908.x	
c1429	62.6	11.0	512	5	BQ388657	NISC_mq03	
1430	62.6	11.0	513	7	CK400174	AGENCOURT	
1431	62.6	11.0	514	6	CA337062	NISC_1v08	
c1432	62.6	11.0	515	5	BO521088	NISC_n109	
1433	62.6	11.0	520	4	BG801745	NISC_1109	
c1434	62.6	11.0	522	7	CF315869	HD--04-P0	
c1435	62.6	11.0	528	5	BQ396638	NISC_ng22	
c1436	62.6	11.0	539	7	CO874827	BOVgen_03	
1437	62.6	11.0	545	7	CK662660	AGENCOURT	
c1438	62.6	11.0	550	5	BQ395636	NISC_ng16	
1439	62.6	11.0	557	4	BM702803	UI-E-CK1-	
c1440	62.6	11.0	559	2	BE964757	601658409	
c1441	62.6	11.0	567	5	BX562696	BX562696	
1442	62.6	11.0	569	6	CB080062	hpb09026.x	
c1443	62.6	11.0	592	2	AM055065	wy99b06.x	
c1444	62.6	11.0	599	7	CO388408	AGENCOURT	
c1445	62.6	11.0	602	5	BQ395529	NISC_ng04	
1446	62.6	11.0	604	1	AV761681	AV761681	
c1447	62.6	11.0	607	7	CO872564	BOVgen_00	
c1448	62.6	11.0	615	5	BQ390276	NISC_mg12	
1449	62.6	11.0	626	7	CF153380	AGENCOURT	
1450	62.6	11.0	633	2	BB795326	BB795326	
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1452	62.6	11.0	664	3	CR718923	Tetracodon	
c1453	62.6	11.0	664	6	CD864037	AZ01.109A	
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1459	62.6	11.0	778	5	BU533438	AGENCOURT	
c1460	62.6	11.0	781	7	CF581396	AGENCOURT	
1461	62.6	11.0	782	1	AV755529	AV755529	
1462	62.6	11.0	786	5	BU535863	AGENCOURT	
1463	62.6	11.0	787	5	BU532114	AGENCOURT	
1464	62.6	11.0	789	5	BU567214	AGENCOURT	
c1465	62.6	11.0	818	2	BE964743	601658288	
1466	62.6	11.0	827	5	BE964743	601658288	
1467	62.6	11.0	830	5	CV075516	AGENCOURT	
c1468	62.6	11.0	848	9	CNS00GMO	AGENCOURT	
c1469	62.6	11.0	850	2	BE250884	601107308	
1470	62.6	11.0	882	5	BU943627	AGENCOURT	
c1471	62.6	11.0	888	2	BE963868	601657636	
c1472	62.6	11.0	896	4	BM416222	OP21309.M	
c1473	62.6	11.0	897	7	CV068642	f2_new.ch	
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1475	62.6	11.0	898	5	BU954099	AGENCOURT	
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c1477	62.6	11.0	902	7	CF581338	AGENCOURT	
c1478	62.6	11.0	909	7	CF581287	AGENCOURT	
c1479	62.6	11.0	921	2	BE964501	601658613	
c1480	62.6	11.0	921	7	CF581238	AGENCOURT	
1481	62.6	11.0	930	2	BF180841	601804967	
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c1484	62.6	11.0	967	7	CF581389	AGENCOURT	
1485	62.6	11.0	977	6	CD511450	CD511450	AGENCOURT
1486	62.6	11.0	984	5	BP380958	BP380958	
c1487	62.6	11.0	1018	4	BM415046	OP20115.M	
c1488	62.6	11.0	1040	2	BE965668	601659721	
1489	62.6	11.0	1056	5	BU525631	AGENCOURT	
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c1491	62.6	11.0	1110	7	CK166502	CK166502	
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c1493	62.6	11.0	1148	7	CF581516	AGENCOURT	
c1494	62.6	11.0	1201	9	CNS01668	AGENCOURT	
c1495	62.6	11.0	1226	2	BF792586	602253729	
c1496	62.6	11.0	1340	4	BI519381	603062186	
c1497	62.6	11.0	1350	2	BE963144	601656950	
c1498	62.6	11.0	1465	4	BI519402	603062214	
c1499	62.6	11.0	1493	2	BF782166	602106343	
c1500	62.6	11.0	1513	2	BE963879	601657647	
ALIGNMENTS							
RESULT 1							
BI822360							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
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/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."							
ORIGIN							
Query Match							
Best Local Similarity							
Matches 501; Conservative							
65							

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Db      1 CGAGCCCCCGGCGCATGAACTGCGG-CCTCTGAGGGCTGTGCTGAGCCCTGCTGCA 59
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Db      60 GCTCCCGCTGCTGCTTTCTTTAGTGGAGCTCGGCCAAGCTGTGGCCAGCTGTGCTGCGC 119
Qy      185 TGGAGTCTGGCGGCGAGCGCGGAGCGGAGCCCTGAGCCAACTCCCTCGGCACTCCCAAC 244
Db      120 TGGAGTCTGGCGGCGAGCGCGGAGCGGAGCCCTGAGCCAACTCCCTCGGCACTCCCAAC 179
Qy      245 CGCTGAAGCTCTGCTGAGCAAGCTGTGGCAATCCCGTGAACCACTCATATGAGAGGCTCC 304
Db      180 CCTGAAGCTCTGCTGAGCAAGCTGTGGCAATCCCGTGAACCACTCATATGAGAGGCTCC 239
Qy      305 AGAAGTGTGTGAGCTGAGCTGTGGTCCCGAGCGGTGGGGGCGCTGAAGGCTTGAAGGCC 364
Db      240 AGAAGTGTGTGAGCTGAGCTGTGGTCCCGAGCGGTGGGGGCGCTGAAGGCTTGAAGGCC 299
Qy      365 TGCTGGGGGGCCCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACACCTGAGGACA 424
Db      300 TGCTGGGGGGCCCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACACCTGAGGACA 359
Qy      425 AGAGCTGTGCCACCCCGAGAGGCTGAAACCCCGCGCGGAGAGACCGTCCATCCCTT 484
Db      360 AGAGCTGTGCCACCCCGAGAGGCTGAAACCCCGCGCGGAGAGACCGTCCATCCCTT 419
Qy      485 CCCCCGGGCCCCCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAAAAAAAAAA 544
Db      420 CCCCCGGGCCCCCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAAAAAAAAAA 479
Qy      545 AAAAAAAAAAAAAAAAAAAAAA 569
Db      480 AAAAAAAAAAAAAAAAAAAAAA 504

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RESULT 2
BI818715
LOCUS      BI818715
DEFINITION BI818715 496 bp mRNA linear EST 04-OCT-2001
            mRNA sequence.
ACCESSION  BI818715
VERSION    BI818715.1 GI:15930265
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 496)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strauberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            DNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            http://image.llnl.gov
            Plate: LLAM11445 row: e column: 09
            High quality sequence stop: 471.
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                /clone="IMAGE:5178608"
                /lab_host="DH10B"
                /clone_11b="NIH_MGC_115"
                /note="Organ: pooled brain, lung, testis; Vector:
                pcMV-SpOEt6; site_1: NotI; site_2: EcoRV (destroyed); RNA

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FEATURES

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Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5178608"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pcMV-SpOEt6; site_1: NotI; site_2: EcoRV (destroyed); RNA

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source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

Query Match 85.1%; Score 485; DB 4; Length 496;
Best Local Similarity 99.0%; Pred. No. 2,6e-82;
Matches 488; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      56 CGCGCGCCCGGAGCCCGCCGCAATGAAGCTGCGCCGCTCTGGGCTGTGCTGCGCC 115
Db      1 CGCGCGCCCGGAGCCCGCCGCAATGAAGCTGCGCCGCTCTGGGCTGTGCTGCGCC 60
Qy      116 TGCTCTGAGCTCCGCTGCTGTTTCTTTAGTGGGCTGCGCCAGCTGTGAGCCAGCTG 175
Db      61 TGCTCTGAGCTCCGCTGCTGTTTCTTTAGTGGGCTGCGCCAGCTGTGAGCCAGCTG 120
Qy      176 TGCTGCTGTGAGTGTGCGCGGAGAGCGCGGAGCCCGGAGACCTGTGACCACTTGGCA 235
Db      121 TGCTGCTGTGAGTGTGCGCGGAGAGCGCGGAGCCCGGAGACCTGTGACCACTTGGCA 180
Qy      236 CCCTCAACCCCGCTGAAGCTCTGTGTGAGCAAGCTGTGGCAATCCCGTGAACCACTTATAG 295
Db      181 CCCTCAACCCCGCTGAAGCTCTGTGTGAGCAAGCTGTGGCAATCCCGTGAACCACTTATAG 240
Qy      296 AGGCTCTCCAGAAAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 355
Db      241 AGGCTCTCCAGAAAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 300
Qy      356 TGAAGCCCTGCTGTGGGGGCGCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACAC 415
Db      301 TGAAGCCCTGCTGTGGGGGCGCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACAC 360
Qy      416 CTGAGGACCAAGAGCTGTGCCACCCGCGAGAGGCTGAAACCCCGCGCGGAGAGACCTGC 475
Db      361 CTGAGGACCAAGAGCTGTGCCACCCGCGAGAGGCTGAAACCCCGCGCGGAGAGACCTGC 420
Qy      476 CATCCCTTCCCGCGGCGCTCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAA 535
Db      421 CATCCCTTCCCGCGGCGCTCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAA 480
Qy      536 AAAAAAAAAAAAAA 548
Db      481 ATTAACAACAAACA 493

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RESULT 3
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LOCUS      BM977626
DEFINITION BM977626 490 bp mRNA linear EST 21-FEB-2003
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            BM977626
ACCESSION  BM977626
VERSION    BM977626.1 GI:19596235
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 490)
            Bonaldo, M.F., Lennon, G., and Soares, M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
            Genome Res. 6 (9), 791-806 (1996)
            MEDLINE 97044477
            PUBMED 8889548
            Contact: McCray, PB
            McCray Lab
            University of Iowa

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/lab host="DH10B"
/clone lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 82.5%; Score 470.4; DB 5; Length 473;
Best Local Similarity 99.8%; Pred. No. 1.6e-79;
Matches 471; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 CGCGCATGAAGCTCGCGCCCTCTGCGGAGCTGCGTGCCCTGTCCTGCACTCCGCT 132
Db 1 CGCGCATGAAGCTCGCGCCCTCTGCGGAGCTGCGTGCCCTGTCCTGCACTCCGCT 60
QY 133 GCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGAGCCCAAGCTGTGCGCTGAGTGG 192
Db 61 GCTGCTTTCTTAAGTGGGCTCGGCCAAGCTGTGAGCCCAAGCTGTGCGCTGAGTGG 120
QY 193 GCGGCGGAGGCGGCGGCGGAGCCCTGCGCAACCCCTCGGCAACCCGCTGAAG 252
Db 121 GCGGCGGAGGCGGCGGCGGAGCCCTGCGCAACCCCTCGGCAACCCGCTGAAG 180
QY 253 CTCTGCTGAGAGCTGCGGAGCTGCGGCAACCACTCATAGAGGAGCTCCAGAAAGTGT 312
Db 181 CTCTGCTGAGAGCTGCGGAGCTGCGGCAACCACTCATAGAGGAGCTCCAGAAAGTGT 240
QY 313 GTGGCTGAGCTGGAGTCCCAAGGCGTGGGAGCCGTGAAGGCGCTGAGGCGCTGAGG 372
Db 241 GTGGCTGAGCTGGAGTCCCAAGGCGTGGGAGCCGTGAAGGCGCTGAGGCGCTGAGG 300
QY 373 GCGCTGACATGTTTGGCTGAGCGGAGACTGAGACATCTACCTGAGAGCAAGAGCTG 432
Db 301 GCGCTGACATGTTTGGCTGAGCGGAGACTGAGACATCTACCTGAGAGCAAGAGCTG 360
QY 433 CCCAGCCGAGGAGGCTGAAAAACCCGCGGAGGAGAGACGTCATCCCTCCCGGCG 492
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QY 493 CCCTCTCAATAAACGTGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAA 544
Db 421 CCCTCTCAATAAACGTGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAA 472

RESULT 7
LOCUS B1819795 496 bp mRNA linear EST 04-OCT-2001
DEFINITION 603041303F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182081 5',
mRNA sequence.
ACCESSION B1819795
VERSION B1819795.1 GI:15931345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 496)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@dsf-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.jnl.gov
Plate: LIML1454 row: f column: 02
High quality sequence start: 6
Location/Qualifiers
1. 496

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGS:5182081"
/lab host="DH10B"
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/note="Organ: pooled brain, lung, testis; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 82.0%; Score 467.4; DB 4; Length 496;
Best Local Similarity 99.4%; Pred. No. 5.8e-79;
Matches 490; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 55 CGCGGCGCCCGGAGCCCGGCGGAGAGAGCTGCGGCGCCCTCTGAGGAGCTCTGAGGCG 114
Db 1 CGCGGCGCCCGGAGCCCGGCGGAGAGAGCTGCGGCGCCCTCTGAGGAGCTCTGAGGCG 59
QY 115 CTGTCTGTGAGCTCCGCTGTCTTTCTTAAGTGGGCTGCGCAAGCTGTGAGCCAGCTT 174
Db 60 CTGTCTGTGAGCTCCGCTGTCTTTCTTAAGTGGGCTGCGCAAGCTGTGAGCCAGCTT 119
QY 175 GTGGCTGCGCTGAGAGTCCGCGGAGGAGGCGGAGGAGCCCTGAGCAACCCCTTCGGC 234
Db 120 GTGGCTGCGCTGAGAGTCCGCGGAGGAGGAGGAGGAGGAGCCCTGAGCAACCCCTTCGGC 179
QY 235 ACCCTAACCCGCTGAAGCTCTGCTGAGAGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGATA 294
Db 180 ACCCTAACCCGCTGAAGCTCTGCTGAGAGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGATA 229
QY 295 GAGGAGCTCCAGAGTGTGTGCTGAGCTGGGTCCCAAGGCGTGGGAGGCGCTGAAGGCC 354
Db 240 GAGGAGCTCCAGAGTGTGTGCTGAGCTGGGTCCCAAGGCGTGGGAGGCGCTGAAGGCC 299
QY 355 CTGAAGGCGCTGTGGGAGCGCTGACAGTGTGCTGAGCGAGACTGAGAGCATCTACA 414
Db 300 CTGAAGGCGCTGTGGGAGCGCGCTGACAGTGTGCTGAGCGAGACTGAGAGCATCTACA 359
QY 415 CCTGAGAGCAAGAGCGTGGCCACCGCGAGGAGCTGAAAAACCCGCGGAGGAGAGCCGT 474
Db 360 CCTGAGAGCAAGAGCGTGGCCACCGCGAGGAGCTGAAAAACCCGCGGAGGAGAGCCGT 418
QY 475 CCATCCCTTCCCGCGGCGCTCTCATATAACGTGTTAAGAGCAAAAAAAAAAAAAA 534
Db 419 CCATCCCTTCCCGCGGCGCTCTCATATAACGTGTTAAGAGCAAAAAAAAAAAAAA 478
QY 535 AAAAAAAAAAAAAA 547
Db 479 AAAAAAAAAAAAAA 491

RESULT 8
LOCUS BQ067622 1059 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6759083 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5755192
5', mRNA sequence.
ACCESSION BQ067622

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BD0067622.1	GI:19896668	EST.	Homo sapiens (human)	Bukayeva; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	1 (bases 1 to 1059)	NIH-MGC	http://mgs.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
			Contact: Robert Strausberg, Ph.D.					
			Email: cgsabers-remail.nih.gov					
			Tissue Procurement: Life Technologies, Inc.					
			cDNA Library Preparation: Life Technologies, Inc.					
			cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
			DNA Sequencing by: Agencourt Bioscience Corporation					
			Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:					
			http://image.lnl.gov					
			Plate: LNL12793					
			row: m					
			column: 17					
			High quality sequence set: 343.					
			Location/Qualifiers					
			1. 1059					
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			/clone="IMAGE:5755192"					
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			/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed and Gruber (Invitrogen). Research genetics tracking code 021. Note: this is a NIH-MGC Library."					
ORIGIN								
Query Match	81.1%;	Score 462.4;	DB 5;	Length 1059;				
Best Local Similarity	99.8%;	Pred. No. 5.2e-78;						
Matches 463;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;				
57	GGCGGCGCCGAGAGCCCGCGGCCATAACTGCGCGCCGCGGGGCTGTCGCGGCTT							
1	GGCGGCGCCGAGAGCCCGCGGCCATAACTGCGCGCCGCGGGGCTGTCGCGGCTT							
117	GTCCTGAGAGCTCCGCTGCTGCTTTCTTATGTCGCGCTCGGCGCAAGCTGTGCGCCAGCTGT							
61	GTCCTGAGAGCTCCGCTGCTGCTTTCTTATGTCGCGCTCGGCGCAAGCTGTGCGCCAGCTGT							
177	CGCTGCGCTGAGAGTGGCGGCGAGAGCGCGGCGCGGAGACCTGTGACCAACCCCTCGGCAC							
121	CGCTGCGCTGAGAGTGGCGGCGAGAGCGCGGCGCGGAGACCTGTGACCAACCCCTCGGCAC							
237	CCTCAACCCGCTGAAGCTCCGCTGAGAGAGAGCTGGGCAATCCCGTGAACCACTCATAGA							
181	CCTCAACCCGCTGAAGCTCCGCTGAGAGAGAGCTGGGCAATCCCGTGAACCACTCATAGA							
297	GGGCTCCCAAGAGTGTGTGCTGAGAGTGTGCGCGAGAGCGCGTGGGGGCGTGAAGGCGCT							
241	GGGCTCCCAAGAGTGTGTGCTGAGAGTGTGCGCGAGAGCGCGTGGGGGCGTGAAGGCGCT							
357	GAAAGCCCTGCTGGGGGCGCTGAGAGTGTGGCTGAAGCGAGAGCTGAAGCATTTACAC							
301	GAAAGCCCTGCTGGGGGCGCTGAGAGTGTGGCTGAAGCGAGAGCTGAAGCATTTACAC							
417	TGAGGACAAACGCTGCGCCACCCGCGAGAGGCTGAAGAACCCCGCGGAGAGAGACCGTCC							
361	TGAGGACAAACGCTGCGCCACCCCGCGAGAGGCTGAAGAACCCCGCGCGGAGAGACCGTCC							

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QY      477 ATCCCTTCCCGGCGCCCTCTCAATAAGTGTTAAGCAA 520
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RESULT 9
LOCUS   BM921624
DEFINITION
AGENCOURT 6707854 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5753142
5', mRNA sequence.
BM921624
BM921624.1 GI:19372003
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1083)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgadps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Cloned by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12788 row: h column: 07
High quality sequence stop: 486.
Location/Qualifiers
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pCMV-SPORT6; Site_1: Nott1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match      80.9%; Score 461; DB 5; Length 1083;
Best Local Similarity 100.0%; Pred. No. 9.6e-78;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
      20 CGGCGCCGAGCCCGCGGCATGAAGCTCCGCCCTCTCGGAGCTCTCGTGGACCTTG 79

QY      118 TCTCGAGCTCGCTGCTGCTTTCTTACTGAGGCTCGGCAAGCCTGAGGCCAGCCTGTC 177
      |||
      80 TCTCGAGCTCGCTGCTGCTTTCTTACTGAGGCTCGGCAAGCCTGAGGCCAGCCTGTC 139

QY      178 GTCGCGCTGAGAGTCGGCGCGGAGCGCGGAGCCGGAGACCTGCGCAACCCCTCGGACCC 237
      |||
      140 GTCGCGCTGAGAGTCGGCGCGGAGCGCGGAGCCGGAGACCTGCGCAACCCCTCGGACCC 199

QY      238 CTCACCTCGCTGAAGCTCTGCTAGAGAGCCTGGGCAATCCCGTGAACCACTCATAGAG 297
      |||
      200 CTCACCTCGCTGAAGCTCTGCTAGAGAGCCTGGGCAATCCCGTGAACCACTCATAGAG 259

QY      298 GGCTCCAGAAAGTGTGTGAGCTGAAGTGTCCCAAGGCGCTGGGAGCGCTGAAGGCGCTG 357

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Db 260 GGCTCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCGTGAAGCCCTG 319
Qy 358 AAGCCCTGCTGGGGGCCCCCTGACAGTGTGTGCTGAGCCGAGACTGAGATCTTACACT 417
Db 320 AAGGCCCCCTGTGGGGGCCCCCTGACAGTGTGTGCTGAGCCGAGACTGAGATCTTACACT 379
Qy 418 GAGGACAAAGACGCTGCTGCCACCCGCGAGAGGCTGAAAAACCCCGCGGGAGAGACCGTCA 477
Db 380 GAGGACAAAGACGCTGCTGCCACCCGCGAGAGGCTGAAAAACCCCGCGGGAGAGACCGTCA 439
Qy 478 TCCCTTCCCGCCGCGCCCTCTCAATAAAGCTGTTAAGAC 518
Db 440 TCCCTTCCCGCCGCGCCCTCTCAATAAAGCTGTTAAGAC 480

RESULT 10
AM974727 550 bp mRNA linear EST 02-JUN-2000
LOCUS EST36817 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
DEFINITION AM974727
ACCESSION AM974727
VERSION AM974727.1 GI:8165915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaepard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johng@tigr.org
Plate: 338
Seq primer: Reverse.
FEATURES
source 1..550
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSKm"

ORIGIN
Query Match 80.3%; Score 457.6; DB 2; Length 550;
Best Local Similarity 99.1%; Pred. No. 4.3e-77;
Matches 460; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 55 CCGCGGCCCCGAGCCCCCGGCGCAGAAAGCTGCGCCCTCTGGGGCTCTGCGGGCC 114
Db 1 CCTTGGCCCCGAGCCCCCGGCGCAGAAAGCTGCGCCCTCTGGGGCTCTGCGGGCC 60

Qy 115 CTGTCCGACAGCTCCGCTGTGCTTTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCCT 174
Db 61 CTGTCCGACAGCTCCGCTGTGCTTTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCCT 120

Qy 175 GTGCGTGGCTGAGTGGCGGGGAGAGCCGCGGACCTGTGGCAACCCCTGGGC 234
Db 121 GTGCGTGGCTGAGTGGCGGGGAGAGCCGCGGACCTGTGGCAACCCCTGGGC 180

Qy 235 ACCCTGAACCGGCTGAGCTCTGTGAGAGCTGGGCATCCCGTGAACCACTCAT 234
Db 181 ACCCTGAACCGGCTGAGCTCTGTGAGAGCTGGGCATCCCGTGAACCACTCAT 240

Qy 295 GAGGGCTCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCGTGAAGGCC 354
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Db 241 GAGGGCTCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCGTGAAGGCC 300
Qy 355 CTGAAGCCCTGTGGGGGCCCCCTGACAGTGTGTGCTGAGCCGAGACTGAGATCTTACA 414
Db 301 CTGAAGCCCTGTGGGGGCCCCCTGACAGTGTGTGCTGAGCCGAGACTGAGATCTTACA 360
Qy 415 CTTGAGACAAAGACGCTGCCACCCGCGAGAGGCTGAAAAACCCCGCGGGAGAGACCGT 474
Db 361 CTTGAGACAAAGACGCTGCCACCCGCGAGAGGCTGAAAAACCCCGCGGGAGAGACCGT 420
Qy 475 CCATCCCTTCCCGCGCCCTCTCAATAAAGCTGTTAAGAC 518
Db 421 CCATCCCTTCCCGCGCCCTCTCAATAAAGCTGTTAAGAC 464

RESULT 11
BI819014 491 bp mRNA linear EST 04-OCT-2001
LOCUS 60303310F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174526 5',
DEFINITION BI819014
ACCESSION BI819014
VERSION BI819014.1 GI:15930564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 491)
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM11434 row: k column: 07
High quality sequence stop: 470.
FEATURES
source 1..491
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5174526"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NOTI; Site_2: EcoRV (destroyed). RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

ORIGIN
Query Match 80.1%; Score 456.4; DB 4; Length 491;
Best Local Similarity 97.5%; Pred. No. 7.2e-77;
Matches 474; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 58 CCGGCCCGAGCCCCCGGCGCATGAAGCTGCGCCCTCTGGGGCTGTGCGCCCTG 117
Db 1 CCGGCCCGAGCCCCCGGCGCATGAAGCTGCGCG -CTCTGGGGCTGTGCGCCCTG 59

Qy 118 TCTGACAGCTCGGCTGCTGCTTTCTTAGTGGGCTGGCCAAAGCTGTGCGCCAGCTGTC 177
Db 60 TCTGACAGCTCGGCTGCTGCTTTCTTAGTGGGCTGGCCAAAGCTGTGCGCCAGCTGTC 119
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QY 178 GCTGCGCTGGAAGTCTGCGCGCGAGAGCGCGGGCCGGAGAACCTTGCGCCAACTCCCTCGGCAAC 237
|||
Db 120 GCTGCGCTGGAAGTCTGCGCGCGAGAGCGCGGGCCGGAGAACCTTGCGCCAACTCCCTCGGCAAC 179
|||
QY 238 CTCAACCCGCTGAAGCTCTGCTGAGAGCAAGCTTGAGCATCCCGTGAACCACTCATAGAG 297
|||
Db 180 CTCAACCCGCTGAAGCTCTGCTGAGAGCAAGCTTGAGCATCCCGTGAACCACTCATAGAG 239
|||
QY 298 GGCCTCCAGAAAGTGTGTGAGCTGAAGCTGGAGTCCCAAGCCGTGAGGGCCGTGAAGCCCTG 357
|||
Db 240 GGCCTCCAGAAAGTGTGTGAGCTGAAGCTGGAGTCCCAAGCCGTGAGGGCCGTGAAGCCCTG 259
|||
QY 358 AAGGCGCTGCTGAGGGGCGCTGAACAGTGTGTGCTGAGCGAGACCTGAGAGCATCTACACT 417
|||
Db 300 AAGGCGCTGCTGAGGGGCGCTGAACAGTGTGTGCTGAGCGAGACCTGAGAGCATCTACACT 359
|||
QY 418 GAGGACAAGACGTGCGCCCAACCGCGAGGGCTGAAAAACCCGCGCGGGAGAGACCGTCCA 477
|||
Db 360 GAGGACAAGACGTGCGCCCAACCGCGAGGGCTGAAAAACCCGCGCGGGAGAGACCGTCCA 419
|||
QY 478 TCCGCTTCCCGCGGCGCTCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAAAAAAAAA 537
|||
Db 420 TCCGCTTCCCGCGGCGCTCTCAATTAACGTGTGTTAAGCAAAAAAAAAAAAAAAAAAAAA 479
|||
QY 538 AAAAAA 543
|||
Db 480 AAACAA 485
|||

RESULT 12	
LOCUS	BI821791
DEFINITION	BI821791 680 bp mRNA
ACCESSION	603035886F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176672 5',
VERSION	BI821791
KEYWORDS	BI821791.1 GI:15933341
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 680)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Stroup

FEATURES

source

Robert Strausberg, Ph.D.
CGAP@remail.nih.gov
Procurement: Life Technologies, Inc.
Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
Sequencing by: Incyte Genomics, Inc.
Distribution: MGC clone distribution information can be
obtained through the I.M.A.G.E. Consortium/ILNL at:
image.ilnl.gov
ILNL1440 row: d column: 17
Library sequence stop: 465.
Location/Qualifiers
1. 680
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5176672"
/lab_host="DH10B"
/clone_1fb="NH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27;
male lung, age 27, and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.

ORIGIN	Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
Query Match	80.0%; Score 456.2; DB 4; Length 680;
Best Local Similarity	95.2%; Pred. No. 7,9e-77;
Matches 492;	Conservative 0; Mismatched 23; Indels 2; Gaps
QY	56 CGCGCGCCCGAGACCCCGCGGACATGAAGCTCCGCGCCCTCTCTGGGGCTCTCTCGGGGCC 11
DB	1 CGCGCGCCCGAGACCCCGCGGACATGAAGCTCCGCGCCCTCTCTGGGGCTCTCTCGGGGCC 60
QY	116 TGTCTCGAGACTTCGCTGCTGCTTTCTTAGTGGGCTTCGCGCAAGCTGTGTGGCCAGCC 17
DB	61 TGTCTCGAGACTTCGCTGCTGCTTTCTTAGTGGGCTTCGCGCAAGCTGTGTGGCCAGCC 12
QY	176 TCGCTCGCTGGAGTTCGCGCGCG-G-GAGGCGGGGGCGGGACCTCGGCCAACCCCTCGGC 23
DB	121 TCGCTCGCTGGAGTTCGCGCGCG-G-GAGGCGGGGGCGGGACCTCGGCCAACCCCTCGGC 180
QY	235 ACCCTGAACCGCGCTGAAGCTCTCTCTCTAGACAGCTCTGGGATCCCGGTAAACACTCTATA 29
DB	181 ACCCTGAACCGCGCTGAAGCTCTCTCTCTAGACAGCTCTGGGATCCCGGTAAACACTCTATA 240
QY	295 GAGGGCTCCCAAGAGTGTGTGGCTGAGCTGGGTCCTCCAGCGGTGGGGGCGGTGAAGCC 35
DB	241 GAGGGCTCCCAAGAGTGTGTGGCTGAGCTGGGTCCTCCAGCGGTGGGGGCGGTGAAGCC 300
QY	355 CTGAAGGCGCTGTGGGGGGCGCTGAACAGCTTTGGCTGAGCCGAGACTGAGACATCTACA 414
DB	301 CTGAAGGCGCTGTGGGGGGCGCTGAACAGCTTTGGCTGAGCCGAGACTGAGACATCTACA 360
QY	415 CCTGAGGACAAAGACGCTGCCACCGCGAGGGCTGAAAACCCCGCGGGGAGAGACGT 474
DB	361 CCTGAGGACAAAGACGCTGCCACCGCGAGGGCTGAAAACCCCGAGCGGGGAGAGACGT 420
QY	475 CCATCCCTTTCCCGGAGCCCTCTCAA-TAAACGTGTGTAGACACAAAAA 533
DB	421 CCATCCCTTTCCCGGAGCCCTCTCTCAAGTAAACGTGTGTAGACGCAAGGAAAGAGAGA 480
QY	534 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570
DB	481 CAAAGAGAAAGACCCAAACCAAGACAGACAAAAACACA 517

RESULT 13	
B1819045	
LOCUS	
DEFINITION	B1819045 961 bp mRNA
ACCESSION	60303316P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174540 5' ,
VERSION	mRNA sequence.
KEYWORDS	B1819045 B1819045.1 GI:15930595 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NIH-MGC http://mgc.nci.nih.gov/..
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Stranberg Ph.D

Email: CGABIS-remail@lsu.edu, Ph.D.
Tissue Procurement: LifeTechnologies@lsu.edu
CDNA Library Preparation: LifeTechnologies@lsu.edu
DNA Sequencing by: [Incyte Genomics, Inc.](mailto:IncyteGenomics@lsu.edu)
Clone distribution: [MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>](mailto:MGC.G.E.Consortium@lsu.edu)
Plate: [LLM1434_row_k_column: 21](mailto:LLM1434_row_k_column:21)
High quality sequence start: 3
High quality sequence stop: 511.

FEATURES

source

Location/Qualifiers

1. .961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174540"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pcwv-sport6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.4%; Score 452.6; DB 4; Length 961;

Best Local Similarity 97.6%; Pred. No. 3.8e-76; Mismatches 9; Indels 3; Gaps 3;

Matches 491; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

QY 63 CCCGAGCCCCCGGCGCATGAAGCTCGCC-GCCCTCTGGGGCTGTGGTGGCCCTGTCT 121
DB 5 CCCCGAGCCCCCGGCGCATGAAGCTCGCCGCCCTCTGGGGCTGTGGTGGCCCTGTCT 64
QY 122 GCAGCTCCGCTGCTCTTTCTTAAGTGGGCTCGGCGCAAGCTGTGGCCAGCTGTGCTG 181
DB 65 GCAGCTCCGCTGCTCTTTCTTAAGTGGGCTCGGCGCAAGCTGTGGCCAGCTGTGCTG 124
QY 182 CGCTGAGTGGGGCGGCGGAGCGGGCGCGGACCTGTGGCAACCCCTGTGGCACTCTCA 241
DB 125 CGCTGAGTGGGGCGGCGGAGCGGGCGCGGACCTGTGGCAACCCCTGTGGCACTCTCA 184
QY 242 ACCCGCTGAAGCTCTCTGCTAGAGCACTGGGCACTCCCGTGAACCACTCATAGAGGCT 301
DB 185 ACCCGCTGAAGCTCTCTGCTAGAGCACTGGGCACTCCCGTGAACCACTCATAGAGGCT 244
QY 302 CCCGAGAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGCTGAAGGCCCTGAAG 361
DB 245 CCCGAGAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGCTGAAGGCCCTGAAG 304
QY 362 CCTGCTGGGGGCGCTGACGTGTTTGGCTGAGCGGAGACTTGAACCTTACCTGAGG 421
DB 305 CCTGCTGGGGGCGCTGACGTGTTTGGCTGAGCGGAGACTTGAACCTTACCTGAGG 364
QY 422 ACAAGAGCTGCGCACCGCGAGGGGCTGAACCCCGCGCGGGGAGAGCGTCAATCCC 481
DB 365 ACAAGAGCTGCGCACCGCGAGGGGCTGAACCCCGCGCGGGGAGAGCGTCAATCCC 423
QY 482 CTTTCCCC-GGCGCTCTCAATTAACGTGTTTAAGACAAATTAATTAATTAATTAATTA 540
DB 424 CTTTCCCCGGGGGCTCTCAATTAACGTGTTTAAGACAAATTAATTAATTAATTAATTA 483
QY 541 AAAAAAAAAAAAAAAAAAAAAA 563
DB 484 ATATTAACAAAAAAAAAAAAAA 506

RESULT 14
BI824102 885 bp mRNA linear EST 04-OCT-2001
LOCUS 603039244F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180195 5',
DEFINITION mRNA sequence.
ACCESSION BI824102
VERSION BI824102.1 GI:15935652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 885)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM1449 row: 9 column: 12
High quality sequence stop: 469.

FEATURES

source

Location/Qualifiers

1. .885
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5180195"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pcwv-sport6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.1%; Score 450.6; DB 4; Length 885;

Best Local Similarity 94.9%; Pred. No. 9.2e-76; Mismatches 24; Indels 2; Gaps 2;

Matches 487; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

QY 56 CGCGCGCCCCGAGCCCCCGGCGCATGAAGCTCGCCGCCCTCTGGGGCTGTGGTGGCCC 115
DB 1 CGCGCGCCCCGAGCCCCCGGCGCATGAAGCTCGCCGCCCTCTGGGGCTGTGGTGGCCC 60
QY 116 TGTCTGAGAGCTCGGCTGCTTTCTTAAGTGGGCTCGGCGCAAGCTGTGGGCGCAGGCTG 175
DB 61 TGTCTGAGAGCTCGGCTGCTTTCTTAAGTGGGCTCGGCGCAAGCTGTGGGCGCAGGCTG 120
QY 176 TCGCTGC-GCTGAGTTC-GGCGCGGAGGCGGGGCGGGAGCCCTGAGCAACCCCTCGG 233
DB 121 TCGCTGCAGTGTGAGTCTGGCGGCGGAGCGGGGCGGGAGCCCTGAGCAACCCCTCGG 180
QY 234 CACCTTCAACCGGCTGAAGCTCTCTGCTGAGAGCTTGGGATCTCCGTTGAACCACTCAT 233
DB 181 CACCTTCAACCGGCTGAAGCTCTCTGCTGAGAGCTTGGGATCTCCGTTGAACCACTCAT 240
QY 294 AGAGGGCTCCCAAGAGTGTGCTGAGAGCTGGGTCCCGAGCGGCTGGGGGCGTGAAGGC 353
DB 241 AGAGGGCTCCCAAGAGTGTGCTGAGAGCTGGGTCCCGAGCGGCTGGGGGCGTGAAGGC 300
QY 354 CCTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGCTGAGAGCTGAGCATCTTAC 413
DB 301 CTTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGCTGAGAGCTGAGCATCTTAC 360
QY 414 ACCTGAGAGCAGAGCTGTGCCACCCGCGAGGCTGAATACCCCGCGGGAGAGACCG 473
DB 361 ACCTGAGAGCAGAGCTGTGCCACCCGCGAGGCTGAATACCCCGCGGGAGAGACCG 420
QY 474 TCCATCCCTTCCCGCGGCGCTCAATTAAGTGTGAAGCAATTAATTAATTAATTAATTA 533
DB 421 TCCATCCCTTCCCGCGGCGCTCAATTAAGTGTGAAGCAATTAATTAATTAATTAATTA 480
QY 534 AAAAAAAAAAAAAAAAAAAAAA 566

Db 481 CCACACCAAGCCACATCACAACCAACAATACAA 513

RESULT 15

LOCUS

DEFINITION	Accession	Source	EST	Date
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III-CF-EN1-aef-n-17-0-UI.s1	UI-CF-EN1	Homo sapiens	cdna	21-FEB-2003

ACCESSION BM977779

KEYWORDS: BM91119.1 GI:19596542 EST.

SOURCE	Homo sapiens (human)
ORGANISM	homo sapiens

Eukaryota; Metazoa:

REFERENCE
1 (bases 1 to 473)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

AUTHORS
Bonaldo, M.F., Lennon, G. and Soares, M.B.

normalization and subtraction: two approaches to facilitate gene discovery

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2005, 21:13:08 ; Search time 39 Seconds
(without alignments)
256.578 Million cell updates/sec

Title: US-09-989-731-408

Perfect score: 502

Sequence: 1 MKLALGLGCVMLSCSSAAA.....QAVGAVKALKALGLTVFG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	81	16.1	496	2	T09931	probable phosphodi
2	79.5	15.8	1381	2	S60004	hypothetical prote
3	77.5	15.4	601	2	T35054	probable transport
4	77	15.3	335	2	T36304	probable anthranil
5	76	15.1	355	2	AD2973	hypothetical prote
6	76	15.1	355	2	G98309	probable ABC trans
7	76	15.1	699	2	H87275	thio-disulfide int
8	76	15.1	732	2	T47269	copper-transportin
9	75.5	15.0	544	2	H72647	hypothetical prote
10	73.5	14.6	331	2	H84358	transport protein
11	73	14.5	502	2	F83553	gamma-glutamyltran
12	73	14.5	584	2	B87315	hypothetical prote
13	73	14.5	1279	2	T13613	succinyl-CoA synth
14	72	14.3	236	2	A56010	amaa1gote-specifi
15	72	14.3	397	2	F97675	succinyl-CoA synth
16	72	14.3	397	2	AE2900	hypothetical prote
17	72	14.3	528	2	D70968	L-serine dehydrata
18	71.5	14.2	462	2	B87634	ATP-dependent Clp
19	71.5	14.2	874	2	AC3070	endopeptidase clp
20	71.5	14.2	887	2	F98216	probable MFS trans
21	71	14.1	440	2	G83368	heat shock protein
22	70.5	14.0	668	2	G85160	hypothetical prote
23	70.5	14.0	831	2	D71409	probable endopepti
24	70	13.9	431	2	C86178	hypothetical prote
25	70	13.9	452	2	T46147	zinc finger protei
26	70	13.9	477	2	D82179	probable multidrug
27	69.5	13.8	244	2	G75653	hypothetical prote
28	69.5	13.8	396	2	G75454	hypothetical prote
29	69.5	13.8	423	2	C70582	probable PPE prote

30	69.5	13.8	455	2	AD0782	probable L-serine
31	69	13.7	170	2	AF3312	hypothetical prote
32	69	13.7	627	2	D75393	serine proteinase,
33	69	13.7	853	2	T36551	probable ATP-depen
34	69	13.7	3295	2	AE0074	probable adhesin x
35	68.5	13.6	335	2	F84336	hypothetical prote
36	68.5	13.6	335	2	AB0575	ferric enterobacti
37	68.5	13.6	1724	2	T18343	P-glycoprotein - S
38	68	13.5	334	2	S16296	ferric enterobacti
39	68	13.5	334	2	AB5558	ferric enterobacti
40	68	13.5	334	2	E90707	ferric enterobacti
41	68	13.5	560	2	F70719	hypothetical prote
42	67.5	13.4	387	2	C75312	branched-chain ami
43	67.5	13.4	1179	2	H82706	hypothetical prote
44	67.5	13.4	1206	2	B87247	probable conserved
45	67.5	13.4	2698	2	B96671	similar to transla
46	67	13.3	218	2	F82220	glyoxylase II faml
47	67	13.3	228	2	D75048	aspartate racemase
48	67	13.3	290	2	S72996	probable glycoprot
49	67	13.3	351	2	S72817	probable glycoprot
50	67	13.3	419	2	AB3519	leucine-specific b
51	67	13.3	636	2	F72736	hypothetical prote
52	67	13.3	724	2	H87423	cation-transportin
53	67	13.3	760	2	AB2225	hypothetical prote
54	67	13.3	840	2	B87467	conserved hypochet
55	66.5	13.2	106	2	F86565	CT483 hypochet
56	66.5	13.2	106	2	C72057	conserved hypochet
57	66.5	13.2	146	2	F72709	hypothetical prote
58	66.5	13.2	180	2	TU0149	zein protein - mal
59	66.5	13.2	243	2	T36637	hypothetical prote
60	66.5	13.2	341	2	I55623	chromoxane A2 rec
61	66.5	13.2	465	2	G02738	PREAC-4 - human
62	66.5	13.2	667	2	T23010	hypothetical prote
63	66.5	13.2	873	2	B53225	ecdysone-induced p
64	66.5	13.2	1510	2	T13634	probable minor tal
65	66	13.1	118	2	S45680	lipid transfer pro
66	66	13.1	310	2	AB0312	lysR-family transc
67	66	13.1	330	2	B82063	chiamin ABC transp
68	66	13.1	337	2	B84133	hypothetical prote
69	66	13.1	638	2	S22490	acetoacetate synth
70	66	13.1	1400	2	B70963	hypothetical prote
71	66	13.1	1467	2	A75564	conserved hypochet
72	65.5	13.0	264	2	D87504	hypothetical prote
73	65.5	13.0	289	2	S70547	sepb protein - Sal
74	65.5	13.0	343	2	F86412	p28N4.25 protein
75	65.5	13.0	361	2	H87700	citrate synthase l
76	65.5	13.0	491	2	C70868	hypothetical prote
77	65.5	13.0	593	2	A10850	pathogenicty isla
78	65.5	13.0	593	2	S70216	slpB protein - Sal
79	65.5	13.0	665	2	G97819	hypothetical prote
80	65.5	13.0	848	2	G87220	heat shock protein
81	65.5	13.0	861	2	D82814	ATP-dependent Clp
82	65	12.9	267	2	F87665	hypothetical prote
83	65	12.9	275	2	B72484	hypothetical prote
84	65	12.9	276	2	T05778	hypothetical prote
85	65	12.9	312	2	H83245	hypothetical prote
86	65	12.9	367	2	AG3649	iron(III)-binding
87	65	12.9	385	2	H70503	alpha-2C-adreneryl
88	65	12.9	461	2	A31237	DNA recombinase (E
89	65	12.9	693	1	JH0265	hypothetical prote
90	65	12.9	845	2	T17291	ankyrin 3, long ap
91	65	12.9	4377	2	A55575	membrane-bound cyc
92	64.5	12.8	184	1	A41331	hypothetical prote
93	64.5	12.8	320	2	F64384	iron compound ABC
94	64.5	12.8	346	2	C87397	hypothetical prote
95	64.5	12.8	385	2	C83174	multidrug-efflux c
96	64.5	12.8	411	2	F84135	hypothetical prote
97	64.5	12.8	480	2	T35214	endoglycosylceram
98	64.5	12.8	482	2	TC7332	conserved hypochet
99	64.5	12.8	529	2	C82487	elastin precursor
100	64.5	12.8	784	2	A26601	NADH dehydrogenase
101	64.5	12.8	905	2	G83314	probable tail leng
102	64.5	12.8	952	2	A99823	

103	64.5	12.8	1022	1	139643	RTX-toxin I - Acti
104	64.5	12.8	1026	2	C30854	probable tail leng
105	64.5	12.8	1026	2	F85692	probable tail comp
106	64.5	12.8	1080	2	H90908	probable tail leng
107	64.5	12.8	1608	2	A28182	hemolysin A - Serr
108	64.5	12.8	1767	2	T00458	hypothetical prote
109	64.5	12.8	2274	2	T30258	adenomatous polypo
110	64	12.7	185	2	B75586	urease accessory p
111	64	12.7	327	2	JC7337	chiazole biosynthe
112	64	12.7	426	2	AH1831	hypothetical prote
113	64	12.7	464	2	H82011	probable outer mem
114	64	12.7	469	2	T35526	probable integral
115	64	12.7	491	2	F81655	conserved hypotet
116	64	12.7	520	2	AD2616	chromosomal replic
117	64	12.7	529	2	D97398	dnna protein (L254
118	64	12.7	569	2	F75381	probable two-compo
119	64	12.7	637	2	C87322	methyl-accepting c
120	64	12.7	635	2	B64752	probable dihydroxy
121	64	12.7	693	2	G91194	DNA helicase RecG
122	64	12.7	693	2	C87575	sensor histidine k
123	64	12.7	704	2	H86041	hypothetical prote
124	64	12.7	2479	2	F87386	conserved hypotet
125	63.5	12.6	82	1	CCP855	cytochrome c551 [v
126	63.5	12.6	82	1	CCP855	50S ribosomal prot
127	63.5	12.6	130	2	A87146	probable methylate
128	63.5	12.6	175	2	G72692	probable dehydroge
129	63.5	12.6	263	2	G70583	ribose transport s
130	63.5	12.6	284	2	AE3547	probable anthranil
131	63.5	12.6	345	2	H72488	D-lactate dehydrog
132	63.5	12.6	353	2	E84393	probable transport
133	63.5	12.6	394	2	B85916	probable transport
134	63.5	12.6	398	2	G91071	proton/sodium-glut
135	63.5	12.6	407	2	B70415	probable choriamat
136	63.5	12.6	411	2	D86973	metal ion efflux m
137	63.5	12.6	432	2	C87586	hypothetical prote
138	63.5	12.6	458	2	A70714	L-serine dehydrata
139	63.5	12.6	458	2	D82974	mercury(II) reduct
140	63.5	12.6	519	2	T06752	flagella-associate
141	63.5	12.6	548	1	F370146	conserved hypotet
142	63.5	12.6	677	2	F83954	nitrous oxide redu
143	63.5	12.6	779	2	T44659	conserved hypotet
144	63.5	12.6	1026	2	F69438	probable tail leng
145	63.5	12.6	1061	2	G90876	large structural p
146	63.5	12.6	1048	1	XPBBA9	pyruvate:ferredoxi
147	63.5	12.6	1157	2	T43259	hypothetical prote
148	63	12.5	177	2	B83906	transpor protein
149	63	12.5	239	2	A83620	arabinogalactan-ii
150	63	12.5	264	2	S52955	hypothetical prote
151	63	12.5	266	2	C70788	phosphate ABC tran
152	63	12.5	307	2	G86839	iron(III) diglirat
153	63	12.5	343	2	AC2129	probable PPE prote
154	63	12.5	358	2	H70857	conserved hypotet
155	63	12.5	380	2	T35953	hypothetical prote
156	63	12.5	387	2	F84392	probable PPE prote
157	63	12.5	391	2	D70922	3-oxoacyl-l-acyl-ca
158	63	12.5	414	2	A89866	probable PPE prote
159	63	12.5	434	2	E70857	hypothetical prote
160	63	12.5	613	2	S27770	hypothetical prote
161	63	12.5	620	2	H82761	sulfur deprivation
162	63	12.5	684	2	T36771	probable integral
163	63	12.5	931	2	AF3276	ATP-dependent c1p
164	63	12.5	932	2	S47597	mult protein homol
165	63	12.5	1157	2	T43258	pyruvate:ferredoxi
166	63	12.5	1677	2	T18344	P-glycoprotein E -
167	62.5	12.5	115	2	F97467	hypothetical prote
168	62.5	12.5	265	2	A48121	retrovirus-related
169	62.5	12.5	288	2	G75613	thiamin biosynthes
170	62.5	12.5	314	2	E87427	conserved phosphor
171	62.5	12.5	361	2	H70785	probable phosphori
172	62.5	12.5	388	2	A97672	N-acetylglucosamin
173	62.5	12.5	388	2	AG2896	hypothetical prote
174	62.5	12.5	401	2	F83179	hypothetical prote
175	62.5	12.5	426	2	C96804	hypothetical prote
176	62.5	12.5	445	2	F81378	probable phospho-s
177	62.5	12.5	511	2	G87609	L-aspartate oxidas
178	62.5	12.5	513	2	T12997	hypothetical prote
179	62.5	12.5	573	2	G75463	O-acetylhomoserine
180	62.5	12.5	601	2	H69274	probable long-chain
181	62.5	12.5	618	2	G83494	hypothetical prote
182	62.5	12.5	685	2	AH3414	soluble lytic mure
183	62.5	12.5	760	1	C2MS	classical compleme
184	62	12.4	98	2	E83763	PTS system, cellub
185	62	12.4	117	2	T12079	non-specific lipid
186	62	12.4	137	2	A72731	hypothetical prote
187	62	12.4	200	2	T05055	hypothetical prote
188	62	12.4	222	2	T37019	probable integral
189	62	12.4	222	2	G84380	hypothetical prote
190	62	12.4	287	2	B72568	hypothetical prote
191	62	12.4	295	2	T36201	probable transcrip
192	62	12.4	338	2	AE3334	metal chelate tran
193	62	12.4	363	2	T34931	hypothetical prote
194	62	12.4	382	2	A70705	probable PE protei
195	62	12.4	382	2	T14336	MD23 protein, iso
196	62	12.4	388	2	UC5316	naringenin-chalcon
197	62	12.4	389	2	G87332	hypothetical prote
198	62	12.4	393	2	AE3503	probable iron-cont
199	62	12.4	407	2	A44374	3-carboxy-cis,cis-
200	62	12.4	426	2	A96000	probable membrane
201	62	12.4	474	2	AB0002	hypothetical prote
202	62	12.4	500	2	AE0103	probable sulfatase
203	62	12.4	535	2	F95343	probable copper ex
204	62	12.4	541	2	T14606	probable sugar tra
205	62	12.4	574	2	H83117	probable ATP-bindl
206	62	12.4	621	2	G83878	L-lactate permease
207	62	12.4	620	2	UH0593	Schwann cell myell
208	62	12.4	641	2	AG2164	hypothetical prote
209	62	12.4	643	2	C87412	ABC transporter, H
210	62	12.4	645	2	G90819	hypothetical prote
211	62	12.4	665	2	A12733	NADH-ubiquinone ox
212	62	12.4	665	2	C97515	soluble lytic tran
213	62	12.4	682	2	AE2702	probable soluble l
214	62	12.4	694	2	F97484	ecdysone-induced p
215	62	12.4	829	2	A32494	puff 74B protein -
216	62	12.4	829	2	A34692	N-chimerin homolog
217	62	12.4	883	2	S04722	glycine cleavage s
218	62	12.4	934	2	T00705	probable ATP-bindl
219	62	12.4	954	2	AE2756	hypothetical prote
220	62	12.4	984	2	E97537	probable bacteriop
221	62	12.4	998	2	T35745	hypothetical prote
222	62	12.4	1025	2	AC0930	probable bacteriop
223	62	12.4	1025	2	AB0836	hypothetical prote
224	62	12.4	1030	2	F66763	ribosomal protein
225	61.5	12.3	124	2	I40348	ribosomal protein
226	61.5	12.3	124	2	I40350	LSU ribosomal prot
227	61.5	12.3	124	2	AF3345	hypothetical prote
228	61.5	12.3	133	2	A70986	hypothetical prote
229	61.5	12.3	145	2	C75590	hypothetical prote
230	61.5	12.3	211	2	T35071	probable membrane
231	61.5	12.3	217	2	AB2665	ribo nuclease HII (
232	61.5	12.3	221	2	T09223	probable oxalate o
233	61.5	12.3	229	2	A97447	hypothetical prote
234	61.5	12.3	257	2	T35711	phosphate transpor
235	61.5	12.3	283	2	D69098	hypothetical prote
236	61.5	12.3	304	2	A87258	D-alanine-D-alanin
237	61.5	12.3	306	2	F64185	hypothetical prote
238	61.5	12.3	313	2	G84289	ferriochrome ABC tr
239	61.5	12.3	333	2	C83785	iron ABC transport
240	61.5	12.3	338	2	E75631	anthranilate phosph
241	61.5	12.3	351	2	S17704	hypothetical prote
242	61.5	12.3	355	2	G72636	uv excision repair
243	61.5	12.3	361	2	T40115	hypothetical prote
244	61.5	12.3	368	2	C87549	probable transmemb
245	61.5	12.3	386	2	AD0842	
246	61.5	12.3	394	2	H91182	
247	61.5	12.3	400	2		
248	61.5	12.3				

249	61.5	12.3	400	2	D86029	probable resistant
250	61.5	12.3	402	2	S47768	hypothetical 43K p
251	61.5	12.3	405	2	C90194	hypothetical prote
252	61.5	12.3	434	1	MMBER3	Ula3 protein - hum
253	61.5	12.3	441	2	B70773	probable thra prot
254	61.5	12.3	445	2	AB2022	hypothetical prote
255	61.5	12.3	503	2	S43017	puromycin resistan
256	61.5	12.3	587	2	S61038	D-lactate dehydrog
257	61.5	12.3	739	2	A55314	glycine-tRNA ligase
258	61.5	12.3	820	2	D83337	probable TonB-depe
259	61.5	12.3	1068	2	T48756	mitochondrial nico
260	61.5	12.3	1492	2	T14652	protein J - Yersin
261	61.5	12.3	1545	2	T14966	phage lambda-relac
262	61.5	12.3	2103	2	G86925	probable polyketid
263	61	12.2	117	2	AB2495	conserved hypochet
264	61	12.2	172	2	AB3528	hypothetical prote
265	61	12.2	185	2	S20593	alcohol dehydrogen
266	61	12.2	207	2	A69069	precortin-6y methy
267	61	12.2	215	2	T44791	probable 2-dehydro
268	61	12.2	247	2	AF2182	hypothetical prote
269	61	12.2	259	1	A69162	gufa protein homol
270	61	12.2	257	2	T36675	probable integral
271	61	12.2	330	2	B37767	stress-inducible p
272	61	12.2	333	2	H81154	ADP-hepseose syntha
273	61	12.2	343	2	H70517	probable lppd prot
274	61	12.2	355	2	AF2746	UDP glucosamine N-
275	61	12.2	355	2	E97527	lpxd protein (U516
276	61	12.2	365	2	C87684	conserved hypochet
277	61	12.2	390	2	T16782	hypothetical prote
278	61	12.2	395	2	H75457	hypothetical prote
279	61	12.2	406	2	F83830	nucleoside transpo
280	61	12.2	419	2	C95091	conserved hypochet
281	61	12.2	419	2	G97958	conserved hypochet
282	61	12.2	420	2	H75395	ABC transporter, p
283	61	12.2	422	2	A96015	probable hydroxypr
284	61	12.2	433	2	C69600	magnesium citrate
285	61	12.2	480	2	E75433	hypothetical prote
286	61	12.2	487	2	B72755	probable antibioli
287	61	12.2	525	2	E87076	probable secreted
288	61	12.2	562	2	T43726	K+-transporting AT
289	61	12.2	582	2	C82961	conserved hypochet
290	61	12.2	589	2	F75398	transporter, sodiu
291	61	12.2	625	2	A26456	nicotinic acetylch
292	61	12.2	802	2	B43735	bcsB protein - Ace
293	61	12.2	920	2	C70668	probable mmpL7 pro
294	61	12.2	1010	1	PX2P2P	H+-exporting ATPas
295	61	12.2	1470	1	EA5323	genome polyprotein
296	60.5	12.1	99	1	R6MXL2	ribosomal protein
297	60.5	12.1	138	2	A32998	chorion protein S1
298	60.5	12.1	144	2	AE3423	hypothetical prote
299	60.5	12.1	192	2	AB3587	hypothetical prote
300	60.5	12.1	203	2	T36327	2-amino-4-hydroxy-
301	60.5	12.1	204	2	AE3302	multiple antibioli
302	60.5	12.1	209	2	T05164	hypothetical prote
303	60.5	12.1	219	2	T18541	moB protein precu
304	60.5	12.1	223	1	S72593	detribiotin synth
305	60.5	12.1	223	2	AB2339	hypothetical prote
306	60.5	12.1	226	2	D87061	hypothetical prote
307	60.5	12.1	233	2	AB0273	probable membrane
308	60.5	12.1	244	2	T29079	hypothetical prote
309	60.5	12.1	259	2	B95335	protein (imported
310	60.5	12.1	260	2	AH0698	probable pathogeni
311	60.5	12.1	260	2	AH0698	hypothetical prote
312	60.5	12.1	297	2	B86766	allergen Poa p IX
313	60.5	12.1	312	2	B39098	NADH dehydrogenase
314	60.5	12.1	312	1	AH0797	1-phosphofructokin
315	60.5	12.1	341	2	JH0606	chromoxane A2 rec
316	60.5	12.1	349	2	AB4306	hypothetical prote
317	60.5	12.1	367	2	AG0555	2-aminoethylphosph
318	60.5	12.1	367	2	T46947	2-aminoethylphosph
319	60.5	12.1	378	2	B75547	iron-sulfur cofact
320	60.5	12.1	383	2	T08705	hypothetical prote
321	60.5	12.1	385	2	T35885	agas protein - Str
322	60.5	12.1	401	2	H70658	probable aroF prot
323	60.5	12.1	405	2	D83351	hypothetical prote
324	60.5	12.1	431	2	AF0276	probable membrane
325	60.5	12.1	432	2	T35729	hypothetical prote
326	60.5	12.1	452	2	T46923	hypothetical prote
327	60.5	12.1	528	2	A41718	polypyrimidine tra
328	60.5	12.1	547	2	A95861	hypothetical prote
329	60.5	12.1	616	2	A40595	methylnalonyl-CoA
330	60.5	12.1	656	2	A72428	methy1-accepting c
331	60.5	12.1	656	2	E72379	methy1-accepting c
332	60.5	12.1	661	2	G72316	methy1-accepting c
333	60.5	12.1	713	2	T19501	hypothetical prote
334	60.5	12.1	715	2	T19500	hypothetical prote
335	60.5	12.1	774	2	A28392	penicillin amidase
336	60.5	12.1	867	2	E86815	ClpB protein (impo
337	60.5	12.1	1273	2	T17188	ClpB protein - ra
338	60.5	12.1	1341	2	T17200	ClpB protein - ra
339	60.5	12.1	1327	2	T25604	hypothetical prote
340	60.5	12.0	127	2	S49537	ribosomal protein
341	60	12.0	130	2	S41123	ribosomal protein
342	60	12.0	130	2	A70615	probable ribosomal
343	60	12.0	157	2	S36784	mucin - rat (fragm
344	60	12.0	179	1	A42840	ribosomal protein
345	60	12.0	181	2	AC2124	hypothetical prote
346	60	12.0	231	2	AE2164	hypothetical prote
347	60	12.0	268	2	B61615	fibroin heavy chai
348	60	12.0	273	2	D71326	conserved hypochet
349	60	12.0	287	2	S45662	histone H1 - comat
350	60	12.0	312	2	AE2953	transcription regu
351	60	12.0	321	2	E86061	D-ribose high-affil
352	60	12.0	321	2	AD0952	high affinity ribo
353	60	12.0	321	2	G65178	high affinity ribo
354	60	12.0	321	2	D91215	high affinity ribo
355	60	12.0	322	2	F83300	probable enoyl-CoA
356	60	12.0	326	2	T50915	hypothetical prote
357	60	12.0	328	2	T40013	thiazole biosynthe
358	60	12.0	336	2	H98329	transcription regu
359	60	12.0	350	2	E64702	cytochrome-c perox
360	60	12.0	352	2	A36128	regulatory protei
361	60	12.0	354	2	T04779	hypothetical prote
362	60	12.0	371	1	S49786	3-isopropylmalate
363	60	12.0	372	1	G82328	aminotransferase,
364	60	12.0	375	1	A42343	alcohol dehydrogen
365	60	12.0	392	2	AE3382	nifs protein [lipo
366	60	12.0	392	2	A49308	nitrite reductase
367	60	12.0	436	2	A13581	selenocysteine lya
368	60	12.0	448	2	T36597	protein F53A3.6 [l
369	60	12.0	451	2	D88395	nitrogenase molybd
370	60	12.0	458	2	A26940	outer membrane pro
371	60	12.0	466	2	A81239	mannose-1-phosphat
372	60	12.0	471	2	AC3622	isocitrate dehydro
373	60	12.0	483	2	A97744	isocitrate dehydro
374	60	12.0	483	2	E71681	phosphotransferase
375	60	12.0	485	2	G65051	UDP-N-acetylmuramo
376	60	12.0	490	2	B87023	mannose-6-phosphat
377	60	12.0	530	2	S30187	conserved hypochet
378	60	12.0	505	2	E83551	variant surface gl
379	60	12.0	517	2	C35480	variant surface gl
380	60	12.0	530	1	G64918	phosphotransferase
381	60	12.0	530	1	G64918	PTS system, maltos
382	60	12.0	530	2	A99920	PTS system, maltos
383	60	12.0	533	1	ORECM2	methy1-accepting c
384	60	12.0	533	1	C90953	methy1-accepting c
385	60	12.0	533	2	G85801	sensor histidine k
386	60	12.0	555	2	A87458	sodium/dicarboxyla
387	60	12.0	593	2	146528	3-methylcrotonyl-C
388	60	12.0	663	2	AF2984	3-methylcrotonyl-C
389	60	12.0	709	2	A98299	subtilisin-like pr
390	60	12.0	761	1	S52769	subtilisin-like pr
391	60	12.0	761	1	C95202	primosomal protein
392	60	12.0	798	2	C98069	primosomal replica
393	60	12.0	798	2	T05602	hypothetical prote
394	60	12.0	820	2		

395	60	12.0	825	2	S26706	transcription fact
396	60	12.0	927	2	A48095	transcription fact
397	60	12.0	1011	2	T50344	poly(A) + RNA trans
398	60	12.0	1012	2	T50300	poly(A) + RNA trans
400	60	12.0	1060	2	S33641	homeotic protein z
401	60	12.0	1122	2	T14180	exit protein - Myc
402	60	12.0	1123	1	NMBEH7	U37 protein - hum
403	60	12.0	1439	2	T02087	gag/pol polyprotei
404	60	12.0	1517	2	T13329	hypothetical prote
405	60	12.0	1533	2	A46221	abdominal segment
406	60	12.0	3938	2	T42761	Bassoon protein -
407	60	12.0	4613	2	T17409	polyketide synthas
408	59.5	11.9	136	2	H70938	hypothetical prote
409	59.5	11.9	139	2	S76129	hypothetical prote
410	59.5	11.9	142	2	H87265	conserved hypotet
411	59.5	11.9	169	2	C75595	hypothetical prote
412	59.5	11.9	230	2	AH0692	conserved hypotet
413	59.5	11.9	247	2	H70432	ABC transporter -
414	59.5	11.9	293	2	G87093	probable transfera
415	59.5	11.9	305	2	AB2464	tRNA delta-2-isope
416	59.5	11.9	327	2	F75573	conserved hypotet
417	59.5	11.9	327	2	C91118	hypothetical prote
418	59.5	11.9	327	2	B85963	hypothetical prote
419	59.5	11.9	328	2	G87391	ABC transporter, A
420	59.5	11.9	341	2	JC4051	Jun-D protein - ra
421	59.5	11.9	352	2	C47293	serine-pyruvate am
422	59.5	11.9	357	2	T01434	NADPH HC toxin red
423	59.5	11.9	357	2	T03970	NADPH HC-toxin red
424	59.5	11.9	363	2	G84385	dipeptide ABC tran
425	59.5	11.9	367	1	DESCDA	aspartate-semialde
426	59.5	11.9	367	1	F91163	aspartate-semialde
427	59.5	11.9	367	2	G86009	aspartate-semialde
428	59.5	11.9	368	2	AB0995	aspartate-semialde
429	59.5	11.9	372	2	AC2952	aspartate-semialde
430	59.5	11.9	372	2	B98331	aspartate-semialde
431	59.5	11.9	383	2	G72777	probable transamin
432	59.5	11.9	389	2	B86017	probable S2P metin
433	59.5	11.9	389	2	B91171	probable 3-oxoacyl
434	59.5	11.9	396	2	T35254	probable 3-oxoacyl
435	59.5	11.9	399	2	D95279	conserved hypotet
436	59.5	11.9	417	2	F90270	probable alcohol
437	59.5	11.9	425	2	T36585	amino acid permeas
438	59.5	11.9	431	2	G82235	probable membrane
439	59.5	11.9	444	1	BE9130	sensor histidine k
440	59.5	11.9	448	1	A26190	histidine-CRNA lig
441	59.5	11.9	448	2	AH1952	glucanase permease
442	59.5	11.9	469	2	H97064	two-component sens
443	59.5	11.9	491	2	T10930	probable sugar-pro
444	59.5	11.9	499	2	A38891	RNA-binding protei
445	59.5	11.9	499	2	G95945	cytochrome-c oxida
446	59.5	11.9	529	2	A95423	probable histidine
447	59.5	11.9	530	2	S15552	polypyrrolidine tra
448	59.5	11.9	536	2	B46230	RNA-binding protei
449	59.5	11.9	538	1	VGNZAM	cell fusion glycop
450	59.5	11.9	538	1	VGNZAM	cell fusion glycop
451	59.5	11.9	538	1	VGNZAM	cell fusion glycop
452	59.5	11.9	538	1	VGNZAM	cell fusion glycop
453	59.5	11.9	538	1	VGNZAM	cell fusion glycop
454	59.5	11.9	538	1	VGNZAM	cell fusion glycop
455	59.5	11.9	538	1	VGNZAM	cell fusion glycop
456	59.5	11.9	538	1	VGNZAM	cell fusion glycop
457	59.5	11.9	538	1	VGNZAM	cell fusion glycop
458	59.5	11.9	538	1	VGNZAM	cell fusion glycop
459	59.5	11.9	538	1	VGNZAM	cell fusion glycop
460	59.5	11.9	538	1	VGNZAM	cell fusion glycop
461	59.5	11.9	538	1	VGNZAM	cell fusion glycop
462	59.5	11.9	538	1	VGNZAM	cell fusion glycop
463	59.5	11.9	538	1	VGNZAM	cell fusion glycop
464	59.5	11.9	538	1	VGNZAM	cell fusion glycop
465	59.5	11.9	538	1	VGNZAM	cell fusion glycop
466	59.5	11.9	538	1	VGNZAM	cell fusion glycop
467	59.5	11.9	538	1	VGNZAM	cell fusion glycop

541	59	11.8	1019	2	AB2136	polyketide synthas
542	59	11.8	1086	1	DEB0XM	NAD(P) transhydrog
543	59	11.8	1136	1	AB1581	different protein
544	59	11.8	3591	1	S21010	filamentous hemaggl
545	58.5	11.7	104	1	CCP85B	cytochrome c551 pr
546	58.5	11.7	130	1	S31143	ribosomal protein
547	58.5	11.7	132	1	E70434	conserved hypochet
548	58.5	11.7	137	2	S42026	acyl carrier prote
549	58.5	11.7	181	2	AF1931	hypochetrical prote
550	58.5	11.7	186	2	D83354	hypochetrical prote
551	58.5	11.7	233	2	T35186	ribonuclease H1 -
552	58.5	11.7	256	2	S07371	histone H1 - fruit
553	58.5	11.7	256	2	E83287	hypochetrical prote
554	58.5	11.7	261	2	B81934	probable tryptopha
555	58.5	11.7	261	2	D81171	tryptophan synthas
556	58.5	11.7	272	2	D87436	2-keto-4-pentenoat
557	58.5	11.7	296	2	A48496	transcription regu
558	58.5	11.7	302	2	F69000	cobalamin biosynth
559	58.5	11.7	312	2	G65000	transcription regu
560	58.5	11.7	312	2	E91025	lysr-type transcri
561	58.5	11.7	325	2	F85869	lysr-type transcri
562	58.5	11.7	325	2	D98282	ribose ABC transpo
563	58.5	11.7	325	2	AE2991	ABC transporter, m
564	58.5	11.7	333	1	C69812	ferriochrome ABC tr
565	58.5	11.7	338	2	AC0711	asparaginase (EC 3
566	58.5	11.7	340	2	AF2896	hypochetrical prote
567	58.5	11.7	340	2	H97671	hypochetrical prote
568	58.5	11.7	343	2	C69212	conserved hypochet
569	58.5	11.7	352	2	AC2760	sodium bile acid s
570	58.5	11.7	352	2	A97541	hypochetrical prote
571	58.5	11.7	353	2	C72479	hypochetrical prote
572	58.5	11.7	384	2	B82973	probable peptidic
573	58.5	11.7	389	2	H82825	transport protein
574	58.5	11.7	400	2	E83675	hypochetrical prote
575	58.5	11.7	412	2	A83129	tyrosyl-tRNA synth
576	58.5	11.7	434	2	S02072	phosphopyruvate hy
577	58.5	11.7	435	2	AD2223	dihydroacetate lim
578	58.5	11.7	451	2	H75559	conserved hypochet
579	58.5	11.7	454	2	H65054	hypochetrical prote
580	58.5	11.7	459	2	B83368	hypochetrical prote
581	58.5	11.7	475	2	D84593	hypochetrical prote
582	58.5	11.7	476	2	H82431	L-serine dehydrata
583	58.5	11.7	492	2	AB4520	probable sucrose-p
584	58.5	11.7	492	2	AD3047	copper tolerance p
585	58.5	11.7	492	2	H98238	hypochetrical prote
586	58.5	11.7	499	2	F70418	conserved hypochet
587	58.5	11.7	511	2	A69369	glutamate synthase
588	58.5	11.7	512	2	AF3628	nitrate reductase
589	58.5	11.7	516	2	F70521	hypochetrical prote
590	58.5	11.7	532	2	E87343	ABC transporter, A
591	58.5	11.7	532	2	D95287	conserved hypochet
592	58.5	11.7	551	2	F83015	hypochetrical prote
593	58.5	11.7	560	2	E70814	probable pdc prote
594	58.5	11.7	575	2	G75282	probable glutathio
595	58.5	11.7	592	2	S46273	tryptophan transpo
596	58.5	11.7	620	2	AF0554	1-deoxyxylulose-5-
597	58.5	11.7	631	2	B42603	beta-glucoside-spe
598	58.5	11.7	634	2	C83530	potassium uptake p
599	58.5	11.7	641	2	T44585	acyl-CoA oxidase h
600	58.5	11.7	682	2	H87409	3-phytase, fusion,
601	58.5	11.7	682	2	H83024	hypochetrical prote
602	58.5	11.7	706	2	H81943	hypochetrical prote
603	58.5	11.7	758	2	JC2521	probable polyribon
604	58.5	11.7	770	2	JC4136	endothelin convert
605	58.5	11.7	787	2	H71453	endothelin convert
606	58.5	11.7	848	2	AF0020	hypochetrical prote
607	58.5	11.7	856	2	C71956	nitrite reductase
608	58.5	11.7	983	2	A87063	probable endopepti
609	58.5	11.7	983	2	A84503	conserved large me
610	58.5	11.7	1008	2	S72698	probable TNP1-like
611	58.5	11.7	1108	2	A48508	transport protein
612	58.5	11.7	1240	1	DJBR21	cyclic-nucleotide
613	58.5	11.7	1256	2	T03096	DNA-directed DNA p
614	58.5	11.7	1438	2	T17402	dhidroaeruginolic
615	58.5	11.7	1607	2	T02837	long chain fatty a
616	58.5	11.7	4957	2	T03455	ALR protein - huma
617	58.5	11.7	5252	2	T03454	ALR protein - huma
618	58	11.6	184	2	E87619	hypochetrical prote
619	58	11.6	191	2	E87253	hypochetrical prote
620	58	11.6	193	2	A48923	major secreted imm
621	58	11.6	193	2	F709320	probable mpt70 pro
622	58	11.6	215	2	A95879	probable dihydroxy
623	58	11.6	222	2	G72459	hypochetrical prote
624	58	11.6	222	2	AD2939	chito1:disulfide in
625	58	11.6	222	2	E98284	in chito1,disulfide in
626	58	11.6	223	2	H75523	hypochetrical prote
627	58	11.6	236	2	B83144	conserved hypochet
628	58	11.6	251	2	AG3116	conserved hypochet
629	58	11.6	255	2	F98170	hypochetrical prote
630	58	11.6	279	1	C42646	dhidropteroate sy
631	58	11.6	279	1	SYECOG	dhidropteroate sy
632	58	11.6	279	2	S07654	dhidropteroate sy
633	58	11.6	279	2	T45123	dhidropteroate sy
634	58	11.6	280	2	C86889	zinc ABC transport
635	58	11.6	283	2	S10928	dhidropteroate sy
636	58	11.6	294	2	A70942	hypochetrical prote
637	58	11.6	297	2	AE2805	permease (imported
638	58	11.6	312	2	E87354	integral membrane
639	58	11.6	318	2	A40944	1-phosphofructokin
640	58	11.6	321	2	E97584	hypochetrical prote
641	58	11.6	323	2	S20099	transforming prote
642	58	11.6	338	2	T46855	anthranilate phosph
643	58	11.6	339	2	E83496	hypochetrical phosph
644	58	11.6	339	2	C95119	iron-compound ABC
645	58	11.6	339	2	G97988	hypochetrical prote
646	58	11.6	340	2	A35630	regulatory protein
647	58	11.6	342	2	AF3357	anthranilate phosph
648	58	11.6	345	2	A70664	hypochetrical prote
649	58	11.6	349	2	B90285	alcohol dehydrogen
650	58	11.6	370	2	F95363	probable serine-py
651	58	11.6	373	1	H71570	alcohol dehydrogen
652	58	11.6	383	2	H71323	probable spore coa
653	58	11.6	386	2	AH3467	glycine betaine/1-
654	58	11.6	390	2	T35206	citrate synthase-1
655	58	11.6	397	2	AF2870	hyd family secret
656	58	11.6	403	2	T04821	hypochetrical prote
657	58	11.6	403	2	H97646	probable membrane
658	58	11.6	408	2	T45721	hypochetrical prote
659	58	11.6	410	2	PN0008	phosphoglycerate K
660	58	11.6	419	2	G70602	hypochetrical prote
661	58	11.6	421	2	E87277	S4 domain protein
662	58	11.6	422	2	B82966	probable phosphat
663	58	11.6	449	2	F91259	hypochetrical prote
664	58	11.6	449	2	B86100	hypochetrical prote
665	58	11.6	449	2	G65214	hypochetrical 45.7
666	58	11.6	460	2	T35539	probable iron-sulf
667	58	11.6	467	2	H82152	PTS system, fructo
668	58	11.6	473	2	C86841	hypochetrical prote
669	58	11.6	480	2	E72471	probable DNA-damag
670	58	11.6	481	2	T10036	hypochetrical prote
671	58	11.6	488	2	T31296	glycolate oxidase
672	58	11.6	491	2	H83979	lysine decarboxyla
673	58	11.6	492	2	B90373	sugar transport re
674	58	11.6	521	1	DNYC27	NADH2 dehydrogenas
675	58	11.6	534	2	A12172	pantothenate synth
676	58	11.6	543	2	A11011	probable membrane
677	58	11.6	543	2	C65209	hypochetrical 59.5
678	58	11.6	543	2	B91246	probable alpha hel
679	58	11.6	543	2	H86093	probable alpha hel
680	58	11.6	544	2	B75541	probable multidrug
681	58	11.6	546	2	C69450	anthranilate synth
682	58	11.6	557	2	T41588	probable amino-aci
683	58	11.6	558	2	G85545	probable transport
684	58	11.6	558	2	C90695	probable transport
685	58	11.6	558	2	E64778	probable membrane
686	58	11.6	579	2	D84137	methyl-accepting c

687	58	11.6	590	2	T42202	probable acyl-CoA
688	58	11.6	590	2	T42206	probable acyl-CoA
689	58	11.6	601	2	E84160	glutamine-fructose
690	58	11.6	638	2	S22491	acetolactate synth
691	58	11.6	693	2	A45456	NADH2 dehydrogenas
692	58	11.6	693	2	A50005	ATP-dependent DNA
693	58	11.6	712	2	AD2721	H+ translocating P
694	58	11.6	714	2	H97502	h+ translocating P
695	58	11.6	725	2	D75294	hypothetical prote
696	58	11.6	754	2	S47268	endothelien-convert
697	58	11.6	904	2	G90563	lipoprotein [import
698	58	11.6	985	2	T29910	hypothetical prote
699	58	11.6	1019	2	T00117	dye protein - fru
700	58	11.6	1322	2	D82685	phosphoribosylform
701	58	11.6	1374	2	T30809	plasmaiogen relate
702	58	11.6	1531	2	T42218	slit-1 protein hom
703	58	11.6	1731	2	AB3045	lice nucleation pro
704	58	11.6	1731	2	B98241	hypothetical prote
705	58	11.6	1744	1	C4HU	complement C4a pre
706	57.5	11.5	111	2	S43115	acidic ribosomal p
707	57.5	11.5	137	2	H70811	hypothetical glyco
708	57.5	11.5	166	2	D69695	ribosomal protein
709	57.5	11.5	214	2	S42244	NADH2 dehydrogenas
710	57.5	11.5	224	1	S74541	negative regulator
711	57.5	11.5	255	1	CPSMMU	muramoylpentapepti
712	57.5	11.5	271	2	T36040	hypothetical prote
713	57.5	11.5	278	2	C75275	hypothetical prote
714	57.5	11.5	287	2	T49329	hypothetical prote
715	57.5	11.5	297	2	S74671	hypothetical prote
716	57.5	11.5	317	2	H75297	conserved hypotet
717	57.5	11.5	323	2	H81951	probable DP-heptos
718	57.5	11.5	323	2	G83461	hypothetical prote
719	57.5	11.5	330	2	H75608	probable acyl-CoA
720	57.5	11.5	331	2	A82267	peptidyl-prolyl ci
721	57.5	11.5	332	2	F75473	conserved hypotet
722	57.5	11.5	336	2	C64329	anthranilate synth
723	57.5	11.5	340	2	S54821	chrb protein - Ew
724	57.5	11.5	363	2	C83128	2,3-butanediol deh
725	57.5	11.5	368	2	G71961	hypothetical prote
726	57.5	11.5	376	2	JC7759	alcohol dehydrat
727	57.5	11.5	383	2	T02642	probable ribening-
728	57.5	11.5	387	2	S16568	ADP-ATP carrier pr
729	57.5	11.5	391	2	A70663	probable PPG prote
730	57.5	11.5	396	2	B75290	hypothetical prote
731	57.5	11.5	417	2	B83487	probable oxidoredu
732	57.5	11.5	428	2	A75423	multitrdng resistn
733	57.5	11.5	445	2	T37161	probable integral
734	57.5	11.5	451	2	G69392	multitrdng resistn
735	57.5	11.5	455	2	A65062	probable integr
736	57.5	11.5	455	2	C85931	L-serine ammonia-1
737	57.5	11.5	455	2	A98086	L-serine dehydrata
738	57.5	11.5	460	2	G82847	hypothetical prote
739	57.5	11.5	460	2	T33110	hypothetical prote
740	57.5	11.5	461	2	S74414	Na+/H+-exchanging
741	57.5	11.5	467	2	F86468	protein F12K21.24
742	57.5	11.5	483	2	T48328	importin alpha-1lk
743	57.5	11.5	504	2	T05543	hypothetical prote
744	57.5	11.5	507	2	B83264	hypothetical prote
745	57.5	11.5	513	2	C95089	ABC transpporter. A
746	57.5	11.5	513	2	P97956	hypothetical prote
747	57.5	11.5	524	2	A64427	cell fusion glycop
748	57.5	11.5	538	1	B60004	conserved hypotet
749	57.5	11.5	576	2	G82792	probable oxaloacet
750	57.5	11.5	593	2	B71373	probable long-chain
751	57.5	11.5	600	2	A87020	glutathione-regula
752	57.5	11.5	617	2	T01227	heat shock protein
753	57.5	11.5	623	2	G81346	chemotaxis methyl-
754	57.5	11.5	678	2	AD2667	hypothetical prote
755	57.5	11.5	678	2	D87607	methy1-accepting c
756	57.5	11.5	715	2	A97449	catlon transpport A
757	57.5	11.5	720	2	D81097	hypothetical prote
758	57.5	11.5	721	2	T41530	probable CCGH-type
759	57.5	11.5	727	2	B84847	
760	57.5	11.5	728	2	H59435	phosphoinositide-3
761	57.5	11.5	756	2	S74929	adenylate cyclase
762	57.5	11.5	794	2	S73328	phorbome lipoprote
763	57.5	11.5	840	1	S69304	pheromone response
764	57.5	11.5	881	2	T03461	methyl-accepting c
765	57.5	11.5	888	2	I58378	tyrosine kinase -
766	57.5	11.5	940	2	A87502	hypothetical prote
767	57.5	11.5	1018	2	T13525	hypothetical prote
768	57.5	11.5	1324	2	S51622	cut3 protein - lts
769	57.5	11.5	2475	2	T00047	gellan lyase (EC 4
770	57	11.4	85	2	A82258	hypothetical prote
771	57	11.4	125	2	D72658	phosphocarrier pro
772	57	11.4	145	2	B82573	hypothetical prote
773	57	11.4	148	2	AD0483	hypothetical prote
774	57	11.4	150	2	E72677	universal stress p
775	57	11.4	158	2	A12718	hypothetical prote
776	57	11.4	158	2	E97500	conserved hypotet
777	57	11.4	172	2	T03380	hypothetical prote
778	57	11.4	207	2	T07854	oleosin 18K - rice
779	57	11.4	216	2	T45430	germin-like protei
780	57	11.4	260	2	C55230	hypothetical prote
781	57	11.4	265	2	T40757	conserved hypotet
782	57	11.4	276	2	E85072	conserved hypotet
783	57	11.4	301	2	G96013	hypothetical prote
784	57	11.4	318	2	AG1441	phosphoglycerate d
785	57	11.4	321	2	A39258	L-arabinose transp
786	57	11.4	321	2	A33635	hypothetical prote
787	57	11.4	325	2	A13635	chitinase biosynthe
788	57	11.4	335	2	B87151	lytB homolog (impo
789	57	11.4	336	2	H72618	hypothetical prote
790	57	11.4	337	2	S29814	glyceraldehide-3-p
791	57	11.4	350	2	F75259	glutamy1-tRNA redu
792	57	11.4	356	2	T01498	NADPH HC toxin red
793	57	11.4	356	2	T01435	NADPH HC toxin red
794	57	11.4	358	2	T64145	probable iron-side
795	57	11.4	358	2	T36415	Sis domain protein
796	57	11.4	365	2	F87315	hypothetical prote
797	57	11.4	366	2	T47001	calcium/proton ant
798	57	11.4	366	2	A10238	alcohol dehydrogen
799	57	11.4	375	1	S66272	probable major tai
800	57	11.4	390	2	AD1035	hypothetical prote
801	57	11.4	392	1	S18593	probable transmemb
802	57	11.4	404	2	E72453	conserved penicilli
803	57	11.4	405	2	T36602	glutamate N-acetyl
804	57	11.4	405	2	A70845	dihydrolipoamide S
805	57	11.4	419	2	G81010	moltydopterin co-f
806	57	11.4	428	2	S73647	hypothetical prote
807	57	11.4	430	2	T44851	O-acetylhomoserine
808	57	11.4	431	2	G70561	probable PG protei
809	57	11.4	437	2	T45481	hypothetical prote
810	57	11.4	437	2	H70918	hypothetical prote
811	57	11.4	445	2	S75859	probable oxidoredu
812	57	11.4	455	2	E91098	hypothetical prote
813	57	11.4	455	2	A85944	hypothetical prote
814	57	11.4	460	2	F83639	conserved hypotet
815	57	11.4	464	2	A75615	hypothetical prote
816	57	11.4	464	2	T36256	probable membrane
817	57	11.4	469	2	B84372	DNA damage-inducib
818	57	11.4	471	2	F82223	sodium/dicarboxyla
819	57	11.4	485	2	C91075	hypothetical prote
820	57	11.4	485	2	B85920	hypothetical prote
821	57	11.4	486	2	A47729	probable ABC trans
822	57	11.4	487	2	T02307	1-aminocyclopropan
823	57	11.4	502	2	S28663	hypothetical glycl
824	57	11.4	514	2	T02307	cytochrome-c oxida
825	57	11.4	524	2	C70558	probable membrane
826	57	11.4	527	1	T02307	probable ABC trans
827	57	11.4	532	2	E75617	sensor histidine k
828	57	11.4	549	2	D64537	L-lactate permease
829	57	11.4	550	1	D69172	DNA-dependent DNA
830	57	11.4	567	2	C75340	probable L-lactate
831	57	11.4	569	2	G95418	hypothetical prote
832	57	11.4	571	2	B86150	

833	57	11.4	575	2	AH2367	two-component syst	906	56.5	11.3	414	2	T51707	hypothetical prote
834	57	11.4	577	2	S72227	finger protein sob	907	56.5	11.3	427	2	A11906	hypothetical prote
835	57	11.4	578	2	D97856	hypothetical prote	908	56.5	11.3	428	2	H97481	probable transmem
836	57	11.4	596	2	G69038	dnax-type molecula	909	56.5	11.3	430	2	F90976	hypothetical prote
837	57	11.4	617	2	T35183	probable ABC-type	910	56.5	11.3	437	2	A38534	branch-chain amyl
838	57	11.4	608	2	C72466	probable translati	911	56.5	11.3	438	2	B64915	probable membrane
839	57	11.4	635	2	G86744	hypothetical prote	912	56.5	11.3	438	2	G85764	probable chloride
840	57	11.4	650	2	E71496	probable sigma reg	913	56.5	11.3	438	2	B90916	glutamate dehydrog
841	57	11.4	693	2	AE0969	ATP-dependent DNA	914	56.5	11.3	449	2	A64053	probable hlyB ABPI
842	57	11.4	724	2	AS3371	glutamate-ammonia	915	56.5	11.3	450	2	E72615	hypothetical prote
843	57	11.4	729	2	AP0458	enoyl-CoA hydratase	916	56.5	11.3	452	2	E72387	hypothetical prote
844	57	11.4	736	2	H75460	conserved hypochet	917	56.5	11.3	454	2	AF0896	L-serine ammonia-1
845	57	11.4	745	2	C83011	hypothetical prote	918	56.5	11.3	462	2	B83123	probable endoprote
846	57	11.4	758	2	AS4667	endoheilin convert	919	56.5	11.3	478	2	C72658	hypothetical prote
847	57	11.4	819	2	F75196	pyruvate, water di	920	56.5	11.3	491	2	T45236	probable membrane
848	57	11.4	844	2	B84773	probable mitochond	921	56.5	11.3	492	2	AD2993	succinoglycan bios
849	57	11.4	856	2	H64552	endopeptidase C1P	922	56.5	11.3	493	2	F98290	exot protein (limpo
850	57	11.4	865	2	D97018	ATPase with chapex	923	56.5	11.3	503	2	H70509	hypothetical prote
851	57	11.4	1021	2	T42566	tegument protein 2	924	56.5	11.3	508	2	AH2688	Na+/H+ antiporter
852	57	11.4	1054	2	T18304	acid trehalase hom	925	56.5	11.3	512	2	AF3402	exopolysphatase
853	57	11.4	1067	2	B87545	AcraB/AcrD/AcrF fam	926	56.5	11.3	518	2	D97310	ATPase component o
854	57	11.4	1067	2	D75625	probable extracell	927	56.5	11.3	520	2	B87621	hypothetical prote
855	57	11.4	1127	2	D70671	pyruvate carboxyla	928	56.5	11.3	525	2	C97470	probable NADH dehy
856	57	11.4	1583	2	T00727	myosin heavy chain	929	56.5	11.3	532	2	B87496	protein-export mem
857	57	11.4	1752	2	A45407	collagen alpha 3(I	930	56.5	11.3	547	2	S26858	isocitrate lyase (
858	57	11.4	2422	2	T12687	MR protein homolo	931	56.5	11.3	547	2	B64963	membrane protein Y
859	57	11.4	3839	2	T49789	related to TOM1 pr	932	56.5	11.3	556	2	C84031	ATP-dependent prot
860	56.5	11.3	130	2	D82620	histone-like prote	933	56.5	11.3	559	2	AD3017	hypothetical prote
861	56.5	11.3	170	2	B75548	transcription regu	934	56.5	11.3	559	2	D98267	ABC transporter AT
862	56.5	11.3	174	2	A35383	superoxide dismuta	935	56.5	11.3	604	2	C90619	NADH dehydrogenase
863	56.5	11.3	207	2	S34234	germin protein - P	936	56.5	11.3	609	2	D75633	conserved hypochet
864	56.5	11.3	208	2	F96750	germin-like protel	937	56.5	11.3	627	2	JC4021	nicotinic acetylch
865	56.5	11.3	212	2	A64045	2-dehydro-3-deoxy	938	56.5	11.3	648	2	T04837	probable serine/th
866	56.5	11.3	227	2	S56941	heat shock protein	939	56.5	11.3	649	2	AF2866	methy1-accepting c
867	56.5	11.3	229	2	B83281	histidine transpor	940	56.5	11.3	670	2	C97643	stimulr to mcpc ge
868	56.5	11.3	237	1	G87541	hypothetical prote	941	56.5	11.3	676	1	WZBE43	gene 43 protein -
869	56.5	11.3	245	2	S62370	conserved hypochet	942	56.5	11.3	688	2	AE0272	probable carbon at
870	56.5	11.3	249	2	A70786	probable Cobs - My	943	56.5	11.3	709	2	AD2843	methy1-accepting c
871	56.5	11.3	258	2	E84037	3-hydroxybutyryl-C	944	56.5	11.3	717	2	E97520	3-phosphatidylinos
872	56.5	11.3	269	2	AP3494	molybdopterin bios	945	56.5	11.3	733	2	B38749	transcription fact
873	56.5	11.3	272	1	A36082	insulin-like growt	946	56.5	11.3	739	1	A34873	DNA helicase/prima
874	56.5	11.3	277	2	S35304	homeotic protein G	947	56.5	11.3	748	2	S61247	probable CDP-alcoh
875	56.5	11.3	286	2	S62370	probable carboxype	948	56.5	11.3	752	2	F84192	phosphoenolpyruvat
876	56.5	11.3	289	2	T25682	hypothetical prote	949	56.5	11.3	773	2	G86856	hypothetical prote
877	56.5	11.3	293	2	AB2295	succinyl-CoA synth	950	56.5	11.3	832	2	B70507	hypothetical prote
878	56.5	11.3	296	2	B83417	hypothetical prote	951	56.5	11.3	902	2	H87323	hypothetical prote
879	56.5	11.3	305	2	S32237	hypothetical prote	952	56.5	11.3	1242	2	T45976	myosin heavy chain
880	56.5	11.3	307	2	B87388	astrohaem synchase	953	56.5	11.3	1434	2	T30172	transmembrane prot
881	56.5	11.3	308	2	B82253	acetyl-CoA carboxy	954	56.5	11.3	1436	2	B70520	probable PPG prote
882	56.5	11.3	308	2	E72627	hypothetical prote	955	56.5	11.3	1536	2	S39510	glutamate synthase
883	56.5	11.3	311	2	T09656	orYR protein homol	956	56.5	11.3	1636	2	S60403	probable membrane
884	56.5	11.3	315	2	T35566	probable integral	957	56.5	11.3	2541	2	S11661	calin - mouse
885	56.5	11.3	316	2	S61237	capsid protein - b	958	56.5	11.3	5762	2	A41819	probable ribosomal
886	56.5	11.3	326	2	D84412	glucose kinase (im	959	56.5	11.2	129	2	B71350	interferon-induced
887	56.5	11.3	337	2	T46958	anthranilate phosp	960	56.5	11.2	130	2	A26316	conserved hypochet
888	56.5	11.3	340	2	A12932	hypothetical prote	961	56.5	11.2	157	2	B87117	probable CDP-alcoh
889	56.5	11.3	344	2	B97687	engat ABC transpor	962	56.5	11.2	186	2	D75005	probable CDP-alcoh
890	56.5	11.3	363	2	AH2796	hypothetical prote	963	56.5	11.2	195	2	T02788	probable ribosomal
891	56.5	11.3	363	2	H97575	probable permease	964	56.5	11.2	197	2	H81184	Na(+)-translocatin
892	56.5	11.3	365	2	C83629	probable permease	965	56.5	11.2	199	1	A38285	interleukin-11 pre
893	56.5	11.3	365	2	A43720	paraoxin hydrolase	966	56.5	11.2	208	1	F69462	hypothetical prote
894	56.5	11.3	375	1	A49107	alcohol dehydrogen	967	56.5	11.2	216	2	S38655	tetr protein - Pse
895	56.5	11.3	379	2	D85823	hypothetical prote	968	56.5	11.2	216	2	J04178	regulatory protein
896	56.5	11.3	389	2	C90215	molybdopterin bios	969	56.5	11.2	220	2	T44702	hypothetical prote
897	56.5	11.3	395	2	C83768	galactokinase (imp	970	56.5	11.2	223	2	AG3288	2-hydroxy-6-oxo-2,
898	56.5	11.3	395	2	T44985	methy1malonyl-CoA	971	56.5	11.2	226	2	C98211	epoxide hydrolase
899	56.5	11.3	399	2	AB0091	probable flagellin	972	56.5	11.2	238	2	AE0006	cRNA nucleotidyltr
900	56.5	11.3	401	2	AC0091	probable flagellin	973	56.5	11.2	245	2	S76632	hypothetical prote
901	56.5	11.3	404	2	A10080	probable flagellin	974	56.5	11.2	256	2	G83232	probable permease
902	56.5	11.3	409	2	AH2659	MFS permease (limpo	975	56.5	11.2	257	2	S16865	gene F41 protein -
903	56.5	11.3	411	2	S47436	flagellar antigen	976	56.5	11.2	260	2	AF3389	cobalamin (5')-phos
904	56.5	11.3	413	2	S55890	plasma protein rec	977	56.5	11.2	267	2	A30988	ly1-1 protein - hu
905	56.5	11.3	413	2	F70560	probable PPG prote	978	56.5	11.2	270	2	C86838	hypothetical prote

979	56	11.2	270	2	T02955	probable cytochrom
980	56	11.2	272	2	D70312	hypothetical prote
981	56	11.2	299	2	E75254	conserved hypothet
982	56	11.2	304	2	B75595	conserved hypothet
983	56	11.2	310	2	D87704	integral membrane
984	56	11.2	325	2	T00686	similar to late em
985	56	11.2	327	2	S30405	hypothetical prote
986	56	11.2	341	2	B71564	probable cationic
987	56	11.2	343	2	F82400	probable hemin ABC
988	56	11.2	347	1	DEP0MW	malate dehydrogena
989	56	11.2	347	1	G97440	hypothetical prote
990	56	11.2	350	2	T12260	caffeoyl-coa O-met
991	56	11.2	350	2	AB1865	hypothetical prote
992	56	11.2	351	2	T50594	probable oxidoredu
993	56	11.2	352	2	G82990	alginatase regulator
994	56	11.2	354	2	AC0389	phosphate binding
995	56	11.2	366	2	AI0647	probable calcium/p
996	56	11.2	367	2	T10088	uroporphyrinogen d
997	56	11.2	369	2	F84291	iron (III) ABC tra
998	56	11.2	370	2	D86957	probable inosine-5
999	56	11.2	373	2	S48451	probable membrane
1000	56	11.2	375	1	S72812	IMP dehydrogenase-
1001	56	11.2	382	2	A72503	hypothetical prote
1002	56	11.2	384	2	AG0149	probable membrane
1003	56	11.2	386	2	H87480	conserved hypothet
1004	56	11.2	392	2	H83198	probable transpo
1005	56	11.2	398	2	AC2911	Mrs permease [impo
1006	56	11.2	406	2	C75537	conserved hypothet
1007	56	11.2	406	2	F70019	nifs protein homol
1008	56	11.2	407	2	T34912	3-oxoacyl-[acyl-ca
1009	56	11.2	415	2	D87020	probable membrane
1010	56	11.2	415	2	T20032	hypothetical prote
1011	56	11.2	424	2	A96014	conserved hypothet
1012	56	11.2	425	2	H84120	methy1-accepting c
1013	56	11.2	433	2	A46231	conserved hypothet
1014	56	11.2	435	2	E82253	he1ix-loop-helix p
1015	56	11.2	441	2	G72579	hypothetical prote
1016	56	11.2	441	2	T17220	hypothetical prote
1017	56	11.2	443	2	A70441	probable PTS syste
1018	56	11.2	451	2	A10955	hemolysin homolog
1019	56	11.2	457	2	B69827	UDP-N-acetylglucos
1020	56	11.2	461	2	G87534	hypothetical prote
1021	56	11.2	462	2	F82012	hypothetical prote
1022	56	11.2	468	2	A70951	two-component sens
1023	56	11.2	472	2	G83932	angiotensin precur
1024	56	11.2	472	2	A29978	RND divalent metal
1025	56	11.2	477	1	F83330	transmembrane prot
1026	56	11.2	486	2	S36190	cytosol aminopepti
1027	56	11.2	486	2	A87459	hypothetical prote
1028	56	11.2	493	2	TC1564	hypothetical prote
1029	56	11.2	511	2	AC3061	hypothetical prote
1030	56	11.2	513	2	D98225	hypothetical prote
1031	56	11.2	513	2	H87022	hypothetical prote
1032	56	11.2	517	2	AB1855	permease protein o
1033	56	11.2	518	2	T35722	probable transport
1034	56	11.2	533	2	G87407	oxidoreductase, GM
1035	56	11.2	540	2	C71969	1-lactate permease
1036	56	11.2	549	2	B82379	conserved hypothet
1037	56	11.2	556	2	A41125	gamma-glutamyltran
1038	56	11.2	561	2	A75874	serine proteinase,
1039	56	11.2	591	2	C90613	NADH dehydrogenase
1040	56	11.2	605	2	T11529	NAH2 dehydrogenas
1041	56	11.2	613	2	T43738	dark-type molecula
1042	56	11.2	613	2	AB1621	class I heat-shock
1043	56	11.2	613	2	AB1258	class I heat-shock
1044	56	11.2	613	2	AB1258	cell cycle histidi
1045	56	11.2	691	2	B87383	hypothetical prote
1046	56	11.2	720	2	T02361	ComC/Rec2 family
1047	56	11.2	725	2	C87485	probable fusidic a
1048	56	11.2	735	2	T35778	snucinojlycan bios
1049	56	11.2	753	2	AB2729	hypothetical prote
1050	56	11.2	753	2	C97510	hypothetical prote
1051	56	11.2	767	2	G96661	hypothetical prote
1052	56	11.2	775	2	AC3400	inorganic diphosph
1053	56	11.2	786	2	E87565	conserved hypothet
1054	56	11.2	790	2	D83011	conserved hypothet
1055	56	11.2	827	2	T20492	hypothetical prote
1056	56	11.2	854	2	D83077	C1ps protein PA454
1057	56	11.2	876	2	E96574	hypothetical prote
1058	56	11.2	947	2	G86420	probable receptor-
1059	56	11.2	977	2	C96745	hypothetical prote
1060	56	11.2	1020	1	W2BE85	gene 23 protein -
1061	56	11.2	1047	1	T41343	probable translati
1062	56	11.2	1086	2	G02257	Mad(p) transhydrog
1063	56	11.2	1151	2	T18535	high molecular mas
1064	56	11.2	1254	1	VHWVVE	structural polypiro
1065	56	11.2	1289	2	T00387	KIAA0622 protein -
1066	56	11.2	1327	2	D70759	probable otsh prot
1067	56	11.2	1398	2	T13741	hypothetical prote
1068	56	11.2	1589	2	T13606	hypothetical prote
1069	56	11.2	1626	2	D72120	hypothetical prote
1070	56	11.2	1839	2	S77626	excinuclease ABC,
1071	55.5	11.1	1839	2	H70316	mannuronan C-5-epi
1072	55.5	11.1	100	2	SYAD93	ATP synthase F0 su
1073	55.5	11.1	138	1	SYAD93	hexon-associated p
1074	55.5	11.1	138	1	SYAD97	hexon-associated p
1075	55.5	11.1	144	2	F84353	enoyl-CoA hydratase
1076	55.5	11.1	161	2	S33624	allophycocyanin be
1077	55.5	11.1	166	2	B44462	allophycocyanin be
1078	55.5	11.1	180	1	S78003	cuticle structural
1079	55.5	11.1	180	1	YOECF7	F17 fibribial prote
1080	55.5	11.1	198	2	AE2534	hypothetical prote
1081	55.5	11.1	199	2	B84259	hypothetical prote
1082	55.5	11.1	200	2	H30203	glutamine amidotra
1083	55.5	11.1	208	2	T43385	60S ribosomal prot
1084	55.5	11.1	211	2	S18463	lysosyme (EC 3.2.1
1085	55.5	11.1	211	2	D69413	conserved hypothet
1086	55.5	11.1	228	2	T08110	germin-like protei
1087	55.5	11.1	231	2	B64920	probable membrane
1088	55.5	11.1	231	2	E80921	hypothetical prote
1089	55.5	11.1	236	2	T36188	hypothetical prote
1090	55.5	11.1	236	2	E70800	probable transport
1091	55.5	11.1	239	2	A42768	homeotic protein g
1092	55.5	11.1	256	1	T17337	hypothetical prote
1093	55.5	11.1	266	2	B82749	4-hydroxybenzoyl-C
1094	55.5	11.1	275	2	E82749	thiamin biosynthes
1095	55.5	11.1	277	2	C70017	probable sugar kin
1096	55.5	11.1	277	2	S73282	hypothetical prote
1097	55.5	11.1	290	2	AD0367	leucyl aminopeptid
1098	55.5	11.1	291	2	AE2416	conserved hypothet
1099	55.5	11.1	292	2	T34997	hypothetical prote
1100	55.5	11.1	295	2	T14912	lysR-type transcri
1101	55.5	11.1	300	2	C83344	leucyl aminopeptid
1102	55.5	11.1	301	2	A75599	conserved hypothet
1103	55.5	11.1	301	2	B64164	ribokinase - Delno
1104	55.5	11.1	304	2	D69744	hypothetical prote
1105	55.5	11.1	305	2	D64963	conserved hypothet
1106	55.5	11.1	305	2	F85823	nitrogen assimilati
1107	55.5	11.1	305	2	H90976	nitrogen assimilati
1108	55.5	11.1	306	2	AG0518	nitrogen assimilati
1109	55.5	11.1	309	2	E72784	D-alanine, D-alanin
1110	55.5	11.1	309	2	B75565	probable dihydroor
1111	55.5	11.1	311	2	D87164	hypothetical prote
1112	55.5	11.1	320	2	AG3543	probable LysR-fami
1113	55.5	11.1	333	2	A33908	acetylglutamate ki
1114	55.5	11.1	336	2	AP1378	allergen Poa p IX
1115	55.5	11.1	337	2	AG1747	B. subtilis ferric
1116	55.5	11.1	341	1	TVMSJD	conserved hypothet
1117	55.5	11.1	342	2	T51703	conserved hypothet
1118	55.5	11.1	346	1	B64976	transforming prote
1119	55.5	11.1	346	2	F90990	nicotinate-nucleot
1120	55.5	11.1	346	2	H85835	galactitol-1-phosp
1121	55.5	11.1	346	2	A84017	galactitol-1-phosp
1122	55.5	11.1	350	2	E71373	immunogenic protei
1123	55.5	11.1	358	2	T43289	probable regulator
1124	55.5	11.1	358	2	T39798	fructose-bisphosph

1125	55.5	11.1	361	2	T27504	hypothetical prote	1198	55.5	11.1	927	2	T00357	hypothetical prote
1126	55.5	11.1	362	2	T14393	probable oleoyl-la	1199	55.5	11.1	946	2	T00024	ent-kaurene syntha
1127	55.5	11.1	365	2	F95857	probable sugar ABC	1200	55.5	11.1	966	2	AH0770	probable membrane
1128	55.5	11.1	374	2	D83328	probable aminotran	1201	55.5	11.1	1020	2	S05944	neuronal cell surf
1129	55.5	11.1	376	1	A26468	alcohol dehydrogen	1202	55.5	11.1	1021	2	A57112	contactin precuro
1130	55.5	11.1	380	2	AB1709	N-acetylglucosamin	1203	55.5	11.1	1030	2	S73944	hypothetical prote
1131	55.5	11.1	384	2	D69471	iron-sulfur bindin	1204	55.5	11.1	1058	2	D82654	ankyrin-like prote
1132	55.5	11.1	388	2	S34672	alkaline serine pr	1205	55.5	11.1	1077	2	A44067	serine-rich protei
1133	55.5	11.1	389	2	E72537	probable cyteine	1206	55.5	11.1	1147	1	MMAX1B	myosin heavy chain
1134	55.5	11.1	395	2	AE1801	D-3-phosphoglycera	1207	55.5	11.1	1236	2	E70937	hypothetical prote
1135	55.5	11.1	395	2	AG1427	D-3-phosphoglycera	1208	55.5	11.1	1263	2	A13338	coBN protein [lmpo
1136	55.5	11.1	400	2	T03460	probable leucine/1	1209	55.5	11.1	1274	2	T18391	lactophillin-3, spl
1137	55.5	11.1	403	1	C69213	protein-export mem	1210	55.5	11.1	1283	2	T18394	lactophillin-3, spl
1138	55.5	11.1	408	2	AC2800	aminotransferase [1211	55.5	11.1	1342	2	T18405	lactophillin-3, spl
1139	55.5	11.1	411	2	B75506	hypothetical prote	1212	55.5	11.1	1351	2	T18409	lactophillin-3, spl
1140	55.5	11.1	416	2	E97579	hypothetical prote	1213	55.5	11.1	1363	1	A55875	xanthine dehydrog
1141	55.5	11.1	418	2	E89772	hypothetical prote	1214	55.5	11.1	1429	2	T13720	gene expanded prot
1142	55.5	11.1	419	1	DEECMB	glycerol-3-phospha	1215	55.5	11.1	1442	2	T42607	transcription acti
1143	55.5	11.1	425	2	AC3391	tetracenomycin c p	1216	55.5	11.1	1442	2	T18538	patched protein -
1144	55.5	11.1	433	2	F75566	probable benzate	1217	55.5	11.1	1491	1	S43793	copper-transportin
1145	55.5	11.1	434	2	E82184	glycerol-3-phospha	1218	55.5	11.1	1556	1	P96587	hypothetical prote
1146	55.5	11.1	449	2	E87639	hypothetical prote	1219	55.5	11.1	1711	1	A47392	chromodomain-helic
1147	55.5	11.1	461	2	S01840	nitrogenase (EC 1.	1220	55.5	11.1	1797	2	T21889	hypothetical prote
1148	55.5	11.1	463	2	T36810	probable integral	1221	55.5	11.1	1805	2	T21888	hypothetical prote
1149	55.5	11.1	476	2	D87386	sodium-dicarboxyla	1222	55.5	11.1	2383	2	D64962	probable membrane
1150	55.5	11.1	485	2	AH0756	probable inner mem	1223	55.5	11.1	2393	2	T17467	riofamycin polyketi
1151	55.5	11.1	486	2	AB1356	amino acid ABC tra	1224	55.5	11.1	5188	2	B85547	probable Rfx fam1
1152	55.5	11.1	486	2	AC1726	amino acid ABC tra	1225	55.5	11.1	5291	2	F90696	hypothetical prote
1153	55.5	11.1	488	2	AB1194	C4-dicarboxylate t	1226	55	11.0	42	2	A37907	hypothetical prote
1154	55.5	11.1	488	2	B81831	probable integral	1227	55	11.0	88	2	AS0238	thymidiotropin beta c
1155	55.5	11.1	493	2	F96696	protein FIN21.12 [1228	55	11.0	107	2	G72496	antifreeze protein
1156	55.5	11.1	498	2	F98149	hypothetical prote	1229	55	11.0	160	2	AE0577	hypothetical prote
1157	55.5	11.1	500	2	E81929	probable phosphate	1230	55	11.0	168	2	E75257	conserved hypochet
1158	55.5	11.1	504	2	G87532	typophan halogen	1231	55	11.0	175	2	S52030	oleosin 17 - maize
1159	55.5	11.1	504	2	T32488	hypothetical prote	1232	55	11.0	178	1	RSR11	ribosomal protein
1160	55.5	11.1	507	2	S64507	probable membrane	1233	55	11.0	179	2	T22734	hypothetical prote
1161	55.5	11.1	513	2	D70836	probable PPE prote	1234	55	11.0	204	2	G83482	probable transcrip
1162	55.5	11.1	518	2	D69813	ABC transporter (A	1235	55	11.0	251	1	G69448	conserved hypochet
1163	55.5	11.1	522	2	T26276	hypothetical prote	1236	55	11.0	252	2	E84083	nitrogen fixation
1164	55.5	11.1	528	2	AC3236	hypothetical prote	1237	55	11.0	253	2	AB3217	3-oxoacyl-(acyl-ca
1165	55.5	11.1	529	2	A69025	translational elonga	1238	55	11.0	253	2	AE2585	molycoprotein bios
1166	55.5	11.1	530	2	G95386	probable Dioxigena	1239	55	11.0	256	2	F83221	beta-ketoacyl redu
1167	55.5	11.1	531	2	T12056	xpsr protein - Xan	1240	55	11.0	271	2	A95267	probable ABC trans
1168	55.5	11.1	533	2	D83468	probable decarboxy	1241	55	11.0	273	2	E75476	hypothetical prote
1169	55.5	11.1	533	2	AB3138	hypothetical prote	1242	55	11.0	277	2	AP2404	hypothetical prote
1170	55.5	11.1	538	2	H83466	probable ATP-bindi	1243	55	11.0	285	2	D97367	moeb-like protein
1171	55.5	11.1	551	2	E64537	L-lactate permease	1244	55	11.0	287	2	G86728	alpha-subunit L-ser
1172	55.5	11.1	551	2	D71969	1-lactate permease	1245	55	11.0	287	2	H70923	probable hg transp
1173	55.5	11.1	559	2	F83283	precortin-3 methyl	1246	55	11.0	302	2	G70614	hypothetical prote
1174	55.5	11.1	560	2	S53382	protein YKR029c ho	1247	55	11.0	308	2	F72704	probable iron (III
1175	55.5	11.1	569	2	SS7812	leucyl aminopeptid	1248	55	11.0	309	2	G83044	lipase lipC PA813
1176	55.5	11.1	570	2	A83118	probable ATP-bindi	1249	55	11.0	318	2	C89775	hypothetical prote
1177	55.5	11.1	582	2	H82393	probable L-lactate	1250	55	11.0	319	2	AB3156	NADP-dependent qui
1178	55.5	11.1	595	2	B97415	hypothetical prote	1251	55	11.0	319	2	G88131	probable NADPH qui
1179	55.5	11.1	595	2	AP2632	conserved hypochet	1252	55	11.0	319	2	S73159	hypothetical prote
1180	55.5	11.1	660	2	H87590	cytochrome c-type	1253	55	11.0	342	2	D83857	anthranilate phosph
1181	55.5	11.1	675	2	S25005	diak-t-type molecula	1254	55	11.0	343	2	F83126	ferric enterobacti
1182	55.5	11.1	689	2	T08988	cadmium-transporti	1255	55	11.0	344	2	T33421	hypothetical prote
1183	55.5	11.1	711	2	A85352	cadmium-transporti	1256	55	11.0	344	2	AD0944	L-rhamnose-proton
1184	55.5	11.1	711	2	T12525	hypothetical prote	1257	55	11.0	344	2	A42436	cellulase (EC 3.2.
1185	55.5	11.1	725	2	F81845	probable cation-tr	1258	55	11.0	359	2	TJ0544	sodium-calcium/pro
1186	55.5	11.1	753	2	T46614	chemotaxis protein	1259	55	11.0	366	2	A99844	sodium-calcium/pro
1187	55.5	11.1	754	2	A53679	endothelin convert	1260	55	11.0	366	2	H85701	hypothetical prote
1188	55.5	11.1	771	2	F70757	probable cation tr	1261	55	11.0	370	2	E75558	coBN protein [lmpo
1189	55.5	11.1	780	2	T00366	hypothetical prote	1262	55	11.0	373	2	C39098	lactophillin-3, spl
1190	55.5	11.1	792	2	C71250	probable cation-tr	1263	55	11.0	375	2	AH0306	lactophillin-3, spl
1191	55.5	11.1	795	2	H70934	5-methyltetrahydro	1264	55	11.0	384	2	A11843	xanthine dehydrog
1192	55.5	11.1	814	2	S65083	probable efflux pr	1265	55	11.0	384	2	D85840	gene expanded prot
1193	55.5	11.1	827	1	T35970	tructose phosphotr	1266	55	11.0	384	2	G90994	transcription acti
1194	55.5	11.1	827	2	T35970	tructose phosphotr	1267	55	11.0	385	2	S64770	hypothetical prote
1195	55.5	11.1	892	2	J00424	probable transposa	1268	55	11.0	389	2	G70769	hypothetical prote
1196	55.5	11.1	903	1	VGBEB1	glycoprotein B pre	1269	55	11.0	390	2	E81062	nitrite reductase
1197	55.5	11.1	904	1	VGBEB7	glycoprotein B pre	1270	55	11.0	391	2	B64307	ammonium transport

1271	55	11.0	392	2	S16206	stilbene synthase
1272	55	11.0	392	2	A87572	aminotransferase
1273	55	11.0	392	2	C96766	hypothetical prote
1274	55	11.0	395	2	AD0380	multidrug efflux p
1275	55	11.0	401	2	C83109	probable transpor
1276	55	11.0	403	2	A81882	probable dihydrol
1277	55	11.0	405	2	F82177	probable multidrug
1278	55	11.0	408	2	G97194	ornithine acetyltr
1279	55	11.0	411	2	S44968	lmbr protein - Str
1280	55	11.0	414	2	T35625	probable sensor-11
1281	55	11.0	418	2	S72761	nitrogen fixation
1282	55	11.0	418	2	AD3417	transporter, mfs s
1283	55	11.0	425	2	E71075	probable proton gl
1284	55	11.0	433	1	B70677	cytochrome P450 Rv
1285	55	11.0	434	2	AB1597	similar glucose in
1286	55	11.0	435	2	F89898	glucose-inhibited
1287	55	11.0	439	2	AP1813	hypothetical prote
1288	55	11.0	441	2	A75619	cobyrinic acid a,c
1289	55	11.0	441	2	S76513	hypothetical prote
1290	55	11.0	449	2	A98239	hypothetical prote
1291	55	11.0	449	2	AC3047	multicopper oxidas
1292	55	11.0	451	2	F82516	chlorophene and fura
1293	55	11.0	459	2	T19110	hypothetical prote
1294	55	11.0	460	2	H87396	conserved hypothet
1295	55	11.0	461	2	JE0030	nitrogenase (EC 1.
1296	55	11.0	466	2	A13262	argininosuccinate
1297	55	11.0	470	2	T46814	gamma-aminobutyrat
1298	55	11.0	470	2	B95419	diaminobutyrate-py
1299	55	11.0	472	2	F82639	resistance protein
1300	55	11.0	474	2	B95847	probable transcrip
1301	55	11.0	475	2	E87225	probable proteinas
1302	55	11.0	476	2	E97228	glu-rNAGin amidol
1303	55	11.0	483	1	VCEP13	hypothetical prote
1304	55	11.0	483	1	T05088	minor coat protein
1305	55	11.0	483	2	E70783	hypothetical prote
1306	55	11.0	495	2	S70171	probable accdp pro
1307	55	11.0	501	2	A32101	integral membrane
1308	55	11.0	509	2	AC1249	glucose transport
1309	55	11.0	520	2	AC1612	hypothetical prote
1310	55	11.0	520	2	J06508	hypothetical prote
1311	55	11.0	531	2	J06508	brahma related gen
1312	55	11.0	531	2	J06508	ribitol kinase [lm
1313	55	11.0	536	2	AH3087	D-ribulokinase (EC
1314	55	11.0	536	2	A99199	hypothetical prote
1315	55	11.0	546	2	E72752	ABC transporter, A
1316	55	11.0	546	2	F87343	hypothetical prote
1317	55	11.0	548	2	G70610	hypothetical prote
1318	55	11.0	554	2	A86211	hypothetical prote
1319	55	11.0	556	2	H83107	polypyrimidine tra
1320	55	11.0	557	2	S68857	pyruvate decarboxy
1321	55	11.0	570	1	UN0782	conserved hypothet
1322	55	11.0	614	2	F89793	feniloyl-coA synth
1323	55	11.0	621	2	H87662	epitroin 2, dragli
1324	55	11.0	627	2	A44112	probable amidase (
1325	55	11.0	642	2	A97555	conserved hypothet
1326	55	11.0	642	2	AC2775	ATPase - pepper (f
1327	55	11.0	660	2	T02755	Fancm1 anemia com
1328	55	11.0	662	2	S58298	transketolase homo
1329	55	11.0	671	2	AC1783	proteinsase IV p2p9
1330	55	11.0	677	2	F96767	neurotrophic recep
1331	55	11.0	685	1	A448289	arginine decarboxy
1332	55	11.0	695	1	S67771	T-box protein 2 -
1333	55	11.0	702	2	G01840	chloride channel 1
1334	55	11.0	797	2	A84308	pyruvate, water di
1335	55	11.0	821	2	T34966	gene 26 protein -
1336	55	11.0	821	2	B71229	calcium-binding pr
1337	55	11.0	837	2	S30971	B. subtilis yueB p
1338	55	11.0	865	2	A47283	calpottin - fruit
1339	55	11.0	865	2	AC1439	nickel-cobalt resi
1340	55	11.0	1067	2	G47056	fibrirogen-binding
1341	55	11.0	1076	2	T30214	DNA-directed DNA p
1342	55	11.0	1092	2	S72213	pyruvate ferredoxi
1343	55	11.0	1116	2	G64310	
1344	55	11.0	1173	2	B97208	
1345	55	11.0	1180	2	A47202	adenylate cyclase
1346	55	11.0	1181	2	A43346	1-phosphatidylinos
1347	55	11.0	1224	1	ERN04H	coatomer complex a
1348	55	11.0	1345	1	VCEB46	major capsid prote
1349	55	11.0	1435	2	S59384	hypothetical prote
1350	55	11.0	1435	2	AC2555	hypothetical prote
1351	55	11.0	1539	2	G70630	probable ctpb prot
1352	55	11.0	1791	2	T02345	hypothetical prote
1353	55	11.0	1821	2	AG2335	hypothetical prote
1354	55	11.0	2437	2	S33611	MIIP1 protein - ra
1355	55	11.0	2629	2	T30987	telomerase-associat
1356	54.5	10.9	57	2	C82891	hypothetical prote
1357	54.5	10.9	100	2	G87478	hypothetical prote
1358	54.5	10.9	108	2	A46222	hypothetical prote
1359	54.5	10.9	111	2	C83320	hydrophobin Ccg-2
1360	54.5	10.9	122	2	S31197	conserved hypothet
1361	54.5	10.9	127	2	A84282	smrB protein - Syn
1362	54.5	10.9	149	2	C72611	hypothetical prote
1363	54.5	10.9	161	1	APF41B	hypothetical prote
1364	54.5	10.9	161	2	A46189	allophycocyanin be
1365	54.5	10.9	162	2	AF1809	hypothetical prote
1366	54.5	10.9	162	2	E71237	hypothetical prote
1367	54.5	10.9	189	2	E71066	vasotocin - Pacifi
1368	54.5	10.9	195	2	G87010	hypothetical prote
1369	54.5	10.9	201	2	G95852	probable membrane
1370	54.5	10.9	208	2	A87269	conserved hypothet
1371	54.5	10.9	220	2	C70525	hypothetical prote
1372	54.5	10.9	227	2	T45209	hypothetical prote
1373	54.5	10.9	228	1	S18588	hypothetical prote
1374	54.5	10.9	241	2	G82391	hypothetical prote
1375	54.5	10.9	247	2	A55717	myelin/oligodendro
1376	54.5	10.9	248	2	F72604	probable high-affi
1377	54.5	10.9	254	2	F70504	hypothetical prote
1378	54.5	10.9	257	2	AH1465	hypothetical prote
1379	54.5	10.9	257	2	E75447	hypothetical prote
1380	54.5	10.9	258	2	T34303	methionine aminope
1381	54.5	10.9	259	2	T34637	probable type IV p
1382	54.5	10.9	275	2	H70860	chiamin biosynthes
1383	54.5	10.9	275	2	H70861	ABC-type iron (III)
1384	54.5	10.9	275	2	H70862	uretic water chan
1385	54.5	10.9	275	2	H70863	inulin-like growt
1386	54.5	10.9	275	2	H70864	probable OXIDOREDU
1387	54.5	10.9	275	2	H70865	probable PE protei
1388	54.5	10.9	275	2	H70866	ABC transporter AT
1389	54.5	10.9	275	2	H70867	lipoprotein (lmpr
1390	54.5	10.9	275	2	H70868	hypothetical prote
1391	54.5	10.9	275	2	H70869	ABC transporter pe
1392	54.5	10.9	275	2	H70870	probable 3-hydroxy
1393	54.5	10.9	275	2	H70871	probable endo alph
1394	54.5	10.9	275	2	H70872	D-alanine-D-alanin
1395	54.5	10.9	275	2	H70873	ADP,ATP carrier pr
1396	54.5	10.9	275	2	H70874	transcription fact
1397	54.5	10.9	275	2	H70875	paired type homeob
1398	54.5	10.9	275	2	H70876	nucleotide sugar e
1399	54.5	10.9	275	2	H70877	aspartate-semialde
1400	54.5	10.9	275	2	H70878	conserved hypothet
1401	54.5	10.9	275	2	H70879	probable polyferr
1402	54.5	10.9	275	2	H70880	glycerolaldehyde-3-p
1403	54.5	10.9	275	2	H70881	flavoprotein (fprA
1404	54.5	10.9	275	2	H70882	anthranilate phosp
1405	54.5	10.9	275	2	H70883	ribase transport s
1406	54.5	10.9	275	2	H70884	lux-related prote
1407	54.5	10.9	275	2	H70885	monooxygenase (lmp
1408	54.5	10.9	275	2	H70886	hypothetical prote
1409	54.5	10.9	275	2	H70887	malate dehydrogena
1410	54.5	10.9	275	2	H70888	hypothetical prote
1411	54.5	10.9	275	2	H70889	hypothetical prote
1412	54.5	10.9	275	2	H70890	Na+/Ca2+-exchangin
1413	54.5	10.9	275	2	H70891	anthranilate phosp
1414	54.5	10.9	275	2	H70892	hemn permease hom
1415	54.5	10.9	275	2	H70893	endoglucanase (lmp
1416	54.5	10.9	275	2	H70894	

1417	54.5	10.9	353	2	F83190
1418	54.5	10.9	354	2	S70595
1419	54.5	10.9	356	2	S71179
1420	54.5	10.9	358	2	C72526
1421	54.5	10.9	360	2	T08581
1422	54.5	10.9	362	2	T38621
1423	54.5	10.9	364	2	T02364
1424	54.5	10.9	368	2	C69590
1425	54.5	10.9	368	2	AD3493
1426	54.5	10.9	376	1	KDBHP
1427	54.5	10.9	378	2	AE0484
1428	54.5	10.9	384	2	H75476
1429	54.5	10.9	387	2	F82398
1430	54.5	10.9	387	2	S14876
1431	54.5	10.9	387	2	S07259
1432	54.5	10.9	390	2	T04096
1433	54.5	10.9	390	2	T49705
1434	54.5	10.9	397	2	T19579
1435	54.5	10.9	398	2	E86923
1436	54.5	10.9	401	2	D82429
1437	54.5	10.9	404	2	T50335
1438	54.5	10.9	413	2	T06325
1439	54.5	10.9	422	2	AD0484
1440	54.5	10.9	422	2	AB1853
1441	54.5	10.9	430	2	C72721
1442	54.5	10.9	431	2	P96764
1443	54.5	10.9	433	2	T19632
1444	54.5	10.9	439	2	B81997
1445	54.5	10.9	439	2	S51378
1446	54.5	10.9	441	2	T31482
1447	54.5	10.9	443	2	G83350
1448	54.5	10.9	458	2	B83341
1449	54.5	10.9	459	2	G69075
1450	54.5	10.9	461	2	C81225
1451	54.5	10.9	462	2	D87630
1452	54.5	10.9	464	2	C75474
1453	54.5	10.9	465	2	T35712
1454	54.5	10.9	465	2	AD2016
1455	54.5	10.9	469	2	AE3353
1456	54.5	10.9	471	2	AE4739
1457	54.5	10.9	471	2	G69809
1458	54.5	10.9	473	1	S18586
1459	54.5	10.9	476	2	T29054
1460	54.5	10.9	486	2	G95865
1461	54.5	10.9	488	2	AH2792
1462	54.5	10.9	488	2	G97571
1463	54.5	10.9	491	2	T27128
1464	54.5	10.9	491	2	E87452
1465	54.5	10.9	493	2	B72704
1466	54.5	10.9	500	2	T35666
1467	54.5	10.9	504	2	S73163
1468	54.5	10.9	508	2	B30310
1469	54.5	10.9	510	2	A70580
1470	54.5	10.9	511	2	S43686
1471	54.5	10.9	524	2	T09937
1472	54.5	10.9	527	2	A13494
1473	54.5	10.9	533	2	G75348
1474	54.5	10.9	535	2	A69537
1475	54.5	10.9	537	2	F84248
1476	54.5	10.9	545	2	C95910
1477	54.5	10.9	549	2	T36879
1478	54.5	10.9	555	2	B87670
1479	54.5	10.9	556	2	S36639
1480	54.5	10.9	560	2	AG2640
1481	54.5	10.9	566	2	T34842
1482	54.5	10.9	566	2	H97422
1483	54.5	10.9	567	2	T52585
1484	54.5	10.9	574	2	T14162
1485	54.5	10.9	592	2	D95383
1486	54.5	10.9	596	2	A28088
1487	54.5	10.9	597	2	E70928
1488	54.5	10.9	607	2	H90054
1489	54.5	10.9	621	2	A82153

probable UDP-3-O-l
NADH2 dehydrogenas
cinamyl-alcohol d
hypothetical prote
cinamyl-alcohol d
probable isopropyl
hypothetical prote
chorismate synthas
leucine- isolenci
thymidine kinase
probable glycerate
probable branched-
ADP,ATP carrier pr
coat protein - tom
glucose-6-phosphat
related to transcr
nccb protein - Alc
conserved hypochet
acetyl-CoA acetyl
mating pheromone r
malate dehydrogena
GntP family permea
hypothetical prote
probable alkylidihy
hypothetical prote
L-serine ammonia-1
probable membrane
hypothetical prote
L-serine dehydrata
nitrogenase molybd
L-serine dehydrata
conserved hypochet
integral membrane
hypothetical prote
L-serine ammonia-1
L-serine ammonia-1
indole-3-acetate b
aminocacid carrier
inactive mercury (I
probable transmemb
probable ribulose-
L-serine dehydrata
1-serine dehydrata
hypothetical prote
ankyrin-related pr
hypothetical prote
probable transcrip
H+-transporting tw
glucose transport
probable UDP-N-ace
monomine transpor
cytokinin oxidase
chromosomal replic
conserved hypochet
cytochrome oxidase
iron transporter-1
probable membrane
probable CRP synth
GGDP family prote
polypyrimidine tra
flagellar M-ring p
probable transfera
flagellar m-ring p
probable nitrate t
hABC transport pro
hypothetical prote
oxalacetate decar
hypothetical prote
conserved hypochet
PTS system, fructo

1490	54.5	10.9	623	2	T35377	probable membrane
1491	54.5	10.9	625	1	H98148	hypothetical prote
1492	54.5	10.9	628	1	S22396	pyruvate synthase
1493	54.5	10.9	634	2	G90779	hypothetical prote
1494	54.5	10.9	637	2	UH0674	L-proline transpor
1495	54.5	10.9	638	2	C64156	hypothetical prote
1496	54.5	10.9	639	2	D82809	exodeoxyribonuclea
1497	54.5	10.9	640	2	F84268	hypothetical prote
1498	54.5	10.9	645	2	A85641	hypothetical prote
1499	54.5	10.9	651	2	AD3139	methyl-accepting c
1500	54.5	10.9	652	2	S50210	surface layer prot

ALIGNMENTS

RESULT 1
T09931
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4.J
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09931
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16897
A:Accession: T09931
A:Molecule type: DNA
A:Residues: 1496 <BEV>
A:Cross-references: UNIPROT:Q9S0B3; EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A:Experimental source: cultivar Columbia; BAC clone T16L4
C:Genetic:
A:Gene: ATSP:T16L4.190
A:Map position: 4
A:Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
C:Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match 16.1%; Score 81; DB 2; Length 496;
Best Local Similarity 41.3%; Pred. No. 5.3;
Matches 26; Conservative 14; Mismatches 17; Indels 6; Gaps 3;

QY 6 LIGLCVALSCSAAPLIVGSAKPVAQPVALLESAAERGA--GTLANPLGLTN-PLKLLLS 62
Db 57 LVTVCIALSAASAFAPLFSSQ--KPVSLINQISKSPAPDRSVAAPLKLKDPVLLIS 113

QY 63 SLG 65
Db 114 SDG 116

RESULT 2
S60004
hypothetical protein - common roundworm retrotransposon R4 (fragment)
C:Species: Ascaris lumbricoideae (common roundworm)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C/Accession: S60004
R:Burke, W.D.; Mueller, F.; Eickbush, T.H.
Nucleic Acids Res. 23, 4628-4634, 1995
A:Title: R4, a non-LTR retrotransposon specific to the large subunit rRNA genes of nematoc
A:Reference number: S60004; MUID:96103592; PMID:8524653
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Accession: S60004
A:Molecule type: DNA
A:Residues: 11381 <BUR>
A:Cross-references: EMBL:U79445; NID:G903660; PID:AAA97394.1; PID:G903661
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Genetic:
A:Genome: retrotransposon

Query Match 15.8%; Score 79.5; DB 2; Length 1381;
Best Local Similarity 27.8%; Pred. No. 21;
Matches 25; Conservative 15; Mismatches 23; Indels 27; Gaps 3;

QY 11 VALSCSAAPLIVGSAKPVAQPVALLESAAERAGT-----LANPLG----- 52

Db 27 IAMPCTNSFPERGTPEHPHPISGTDSSESLSKMGTHRSPLNDDEVINGPKGHESDPVH 86
Qy 53 -----TLNPLKLLSLGIPVNHLEGSQ 76
Db 87 VVRAPRTLHPRL---ELPIGVNLTGEASQ 113

RESULT 3

T35054
probable transport system permease protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35054
R/Seeger, K.U.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A/Reference number: Z21566
A/Accession: T35054
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-601 <SEB>
A/Cross-references: UNIPROT:Q86691; EMBL:AL031371; PIDN:CA20556.1; GSPDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Map position: SCOE:DB:SC4G2.19

Query Match 15.4%; Score 77.5; DB 2; Length 601;
Best Local Similarity 30.7%; Pred. No. 14;

Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;

Qy 3 LAALIGLVALSCSSAAAFVGSAA--KVA-----QPVAALESAAAGAG-----45
Db 426 LVALLVTAVAGSGATPTLAVGAVAMAPLAAHTSSLLRQERATLITATKGLGAGPVHL 485
Qy 46 -----TLANPLGTINPLKLLSLGIPVNHLEGSQKCVAAELGPQ 85
Db 486 RHELLPAVVPVPLRHALLRLPGVALALASGLGLGAGPPSPMGCLLAENQPIAERAPW 545
Qy 86 AVGAVKALKALLGALTIV 102
Db 546 AVLAAPAVALMLGLALAV 562

RESULT 4

T36304
probable anthranilate phosphoribotransferase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T36304
R/Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, March 1999
A/Reference number: Z21604
A/Accession: T36304
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-335 <SAU>
A/Cross-references: UNIPROT:Q924W9; EMBL:AL035654; PIDN:CA38583.1; GSPDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Map position: SCOE:DB:SC8.05C

Query Match 15.3%; Score 77; DB 2; Length 335;
Best Local Similarity 34.5%; Pred. No. 8.3;

Matches 30; Conservative 9; Mismatches 36; Indels 12; Gaps 4;

Qy 7 LGLCVALLSCSSAAAFVGSAA-----KPAVAPVALESAA-----EGAGTIANPGLTNP 56
Db 117 LGVRIDLGAEAAACLDRTGRTFLPAVFNH--AFRHTAGRRRELGAATVFNLLGPICLNP 174
Qy 57 LKLLSSLGIPVNHLEGSQKCVAAELG 83
Db 175 SGARLTILGVPSRELVEPMTETLERTLG 201

RESULT 5

AD2973
hypothetical protein Atcu3389 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AD2973
R/Mood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Moo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A/Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; WUID:21608550; PMID:11743193
A/Accession: AD2973

A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-355 <KUR>
A/Cross-references: UNIPROT:Q8UA14; GB:AE008689; PIDN:AAL44202.1; PID:g17741781; GSPDB:GN

A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;
Best Local Similarity 23.3%; Pred. No. 11;

Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

Qy 2 KLAALIGLVALSCSSAAAFVGSAAKPAVAPVALESAAAGAGTIANPLGTINPLKLL 61
Db 24 KILIVGLFLALCFGMADMLGPARRYTLSEVLA-----TIDPAVAGVQLRVVI 73
Qy 62 SLSGIPVNHLEGSQKCVAA-----ELGPQAVGAVKALKALLGALTIV 103
Db 74 WDIRMPIALMAVTGASLSVAGAQMTILSNPLASPTTLGISAAASFGAALALVGVAIIF 133

RESULT 6

G98309
probable ABC transporter permease protein WU0087 AGR_L_2865 [imported] - Agrobacterium tu
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: G98309
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappae, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; WUID:21608551; PMID:11743194
A/Accession: G98309
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-355 <KUR>

A/Cross-references: UNIPROT:Q8UA14; GB:AE007870; PIDN:AAK90001.1; PID:g15159970; GSPDB:GN
C/Genetics:
A/Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;
Best Local Similarity 23.3%; Pred. No. 11;

Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

Qy 2 KLAALIGLVALSCSSAAAFVGSAAKPAVAPVALESAAAGAGTIANPLGTINPLKLL 61
Db 24 KILIVGLFLALCFGMADMLGPARRYTLSEVLA-----TIDPAVAGVQLRVVI 73
Qy 62 SLSGIPVNHLEGSQKCVAA-----ELGPQAVGAVKALKALLGALTIV 103
Db 74 WDIRMPIALMAVTGASLSVAGAQMTILSNPLASPTTLGISAAASFGAALALVGVAIIF 133

RESULT 7

RESULT 11
Probable aldehyde dehydrogenase PA0747 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: F83553
R/Cloner, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llm,
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: F83553
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-502 <STO>
A/Cross-references: UNIPROT:Q91512; GB:AE004509; GB:AE004091; NID:G9946622; PIDN:AA60413
C/Genetics:
A/Experimental source: strain PA01
A/Gene: PA0747
C/Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 14.5%; Score 73; DB 2; Length 502;
Best Local Similarity 29.1%; Pred. No. 30;
Matches 32; Conservative 13; Mismatches 41; Indels 24; Gaps 5;

QY 4 AALLGLCVALLSCSSA-----AFLVGSAR-----PVAQPVAALES-----AAGAGTL 47
DB 264 AOVGLNVGASCGAQRCAISAAVFAVGAAREMPELAERVAVLRPHQDPDAAYGFL 323
QY 48 ANPLGLTNPGLKLLSLGIPVNHLEGSQKVAE-----LGPVAVAV 90
DB 324 ISFOARQRYVRLIAEGKAGACGLDGSQ-CVGEISYVGNWLGFLPRAY 372

RESULT 12
B87315
Gamma-glutamyltransferase [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: B87315
R/Nierman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heideberg, J.
n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.D.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: B87315
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-584 <STO>
A/Cross-references: UNIPROT:Q9AAR5; GB:AE005673; NID:G13421716; PIDN:AAK22518.1; GSPDB:G
A/Genetics: CC0531
C/Superfamily: gamma-glutamyltransferase

Query Match 14.5%; Score 73; DB 2; Length 584;
Best Local Similarity 28.6%; Pred. No. 35;
Matches 28; Conservative 10; Mismatches 38; Indels 22; Gaps 2;

QY 2 KLAALLGLCVALLSCSSAAAFIVGSAPVQAPV--AALSSAAEAGAGTLANPLGLTNPGLK 59
DB 7 RLASLLALSMALQLSLAPVAALESIPLMPPRRRAAISTAKGVAAANPLAVEAGLAV 66
QY 60 LLSLSLGI PVNHLIEGSKQVAAELGPQAVGAKALKAL 97
DB 67 LRD-----GGSAVDAVAIVAVL 84

RESULT 13
T13613
Hypothetical protein 8D8.2 - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T13613
R/Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A/Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
A/Reference number: Z17695
A/Accession: T13613
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1279 <PAP>
A/Cross-references: UNIPROT:O46099; EMBL:AL022018; NID:e1273253; PID:e1426350; PIDN:CAAT
C/Genetics:
A/Cross-references: Flybase:FBgn0024367
A/Introns: 65/2
A/Note: EG:8D8.2

Query Match 14.5%; Score 73; DB 2; Length 1279;
Best Local Similarity 31.6%; Pred. No. 77;
Matches 31; Conservative 12; Mismatches 29; Indels 26; Gaps 4;

QY 25 SAKVAPVAALES-----AAGAGTLANPLGLTNPGLKLLSLGIPVN 69
DB 213 SANPAAAPAAAFSSHYSAKNAQFLRKPSPGGGGLSS---TVKTVADILSLGIVSG 269
QY 70 HLIEGSK-----CVAELGPQ-AVGAVKALKALGA 99
DB 270 GKSDAHKRYALDDYPALESAPQPSVAVADVADLKLGLHA 307

RESULT 14
A56010
amstgore-specific protein A2 precursor - *Leishmania donovani* infantum
C/Species: *Leishmania donovani* infantum
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C/Accession: A56010
R/Charast, H.; Matlaehewski, G.
Mol. Cell. Biol. 14, 2975-2984, 1994
A/Title: Developmental gene expression in *Leishmania donovani*: differential cloning and
A/Reference number: A56010; MUID:94217695; PMID:754921
A/Accession: A56010
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-236 <CHA>
A/Cross-references: UNIPROT:Q26351; GB:S69693; NID:G546453; PID:G546454
C/Superfamily: proline-rich protein
C/Keywords: tandem repeat

Query Match 14.3%; Score 72; DB 2; Length 236;
Best Local Similarity 29.8%; Pred. No. 17;
Matches 31; Conservative 15; Mismatches 42; Indels 16; Gaps 4;

QY 1 MKLAALLGLCVALLSCSSAAAFIVGSAPV--VAQPVAALESAAEAGAGTLANPLGLTNPGLK 58
DB 1 MKIRSVRLVAVLVVAVLALASAEPRKAAVVGPL-SVGQSVGPLSVGPQAVGFLS 59
QY 59 LLSLSLGI PVNHLIEGSKQVAAELGPQAVGAKALKALKALGATV 102
DB 60 VGQSVG-PLS-----VGQAVGRLSVGQSVGFLS 90

RESULT 15
F97675
succinyl-CoA synthetase beta chain (AF326913) [imported] - *Agrobacterium tumefaciens* (str
C/Species: *Agrobacterium tumefaciens*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
C/Accession: F97675
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman,
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: F97675
A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-397 <KUR>
 A:Cross-references: UNIPROT:Q8UC60; GB:AE007869; PIDN:AK88359.1; PID:G15157842; GSPDB:G
 C;Genetic:
 A:Gene: AGR_C_4780
 A:Map position: circular chromosome
 C/Superfamily: Succinyl-CoA synthetase, beta subunit

Query Match 14.3%; Score 72; DB 2; Length 397;
 Best Local Similarity 36.2%; Pred. No. 29;
 Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

Qy	18	AAAFIVGSAPVAPVALE-SAAEAGGTIANPLGTINPLKLLSSIGIPVNHLEGSQ	76
Db	8	AKALLKGYGAPVPAEGVAHLKVEEAAAKQLPGLVY---VKSQIHAGS-----RKG	57
Qy	77	KCVAEIGPQAVGAVKALKAL	96
Db	58	K-FKEIGPDAKGGVRLAKSI	76

Search completed: March 5, 2005, 21:23:52
 Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 21:19:33 ; Search time 176 Seconds
(without alignments) 302.592 Million cell updates/sec

Title: US-09-989-731-408
Perfect score: 502
Sequence: 1 MKLAALIGLVALSCSSAAA.....QAVGAVKALKALGALTVEG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	104	1	UGR2_HUMAN
2	261	52.0	104	1	Q71MT8
3	250	49.8	104	1	UGR2_MOUSE
4	232	46.2	93	2	Q7M741
5	225	44.8	94	2	Q8C0C6
6	160	31.9	93	1	UGR1_HUMAN
7	148.5	29.6	93	2	Q71MT7
8	135	26.9	139	1	UGR1_MOUSE
9	88	17.5	255	2	Q82LH6
10	83.5	16.6	281	2	Q8FST3
11	83	16.5	1327	1	TNKL_HUMAN
12	82.5	16.4	247	2	Q9K3G4
13	82.5	16.4	694	2	Q98CR1
14	82	16.3	117	2	Q6H4X3
15	82	16.3	540	2	Q62CFO
16	82	16.3	340	2	Q63KM9
17	81	16.1	3	2	Q6AFG5
18	81	16.1	496	2	Q9SU83
19	80	15.9	148	2	Q8XW23
20	79	15.7	136	2	Q82R50
21	79	15.7	176	2	Q61E83
22	78	15.5	344	2	Q7P4X9
23	77.5	15.4	229	2	Q7VY41
24	77.5	15.4	229	2	Q7WA34
25	77.5	15.4	229	2	Q7WJ66
26	77.5	15.4	601	2	Q86691
27	77	15.3	189	2	Q64UD8
28	77	15.3	335	1	TRD2_STTCCO
29	77	15.3	453	1	Q8THL0
30	77	15.3	719	2	Q63RH3
31	76	15.1	355	2	Q8UA14
32	76	15.1	529	2	Q62IX9
33	76	15.1	546	2	Q63SM0
34	76	15.1	609	2	Q9ABL0
35	76	15.1	732	1	COPA_HELPF
36	76	15.1	889	1	CLPB_BIPLO
37	75.5	15.0	459	2	Q9F2I6
38	75.5	15.0	496	2	Q8G3S2
39	75.5	15.0	544	2	Q9YEG2
40	75.5	15.0	667	2	Q8XRM8
41	75	14.9	299	2	Q89XU3
42	75	14.9	355	2	Q8RFX3
43	75	14.9	362	1	MEDI_HUMAN
44	75	14.9	362	1	MEDI_MOUSE
45	75	14.9	370	2	Q89H46
46	75	14.9	463	2	Q8C313
47	75	14.9	574	2	Q6FQW0
48	74.5	14.8	331	2	Q6N849
49	74.5	14.8	398	2	Q69UA9
50	74	14.7	283	2	Q75D55
51	74	14.7	547	2	Q6M849
52	74	14.7	611	2	Q91OK1
53	74	14.7	779	1	SNIL_MOUSE
54	73.5	14.6	119	2	Q86D11
55	73.5	14.6	242	2	Q757F5
56	73.5	14.6	331	2	Q9HNI9
57	73.5	14.6	358	2	Q8NQ28
58	73.5	14.6	389	2	Q8EJ01
59	73.5	14.6	422	2	Q6AN39
60	73.5	14.6	626	1	DXS_WIGBR
61	73.5	14.6	776	1	SNIL_RAT
62	73.5	14.6	882	1	SYA_THER2
63	73.5	14.6	882	1	SYA_THER1
64	73.5	14.6	1468	2	Q9GHB5
65	73	14.5	317	2	Q9BD48
66	73	14.5	429	2	Q82SM1
67	73	14.5	67	2	Q91512
68	73	14.5	526	2	Q6NHX3
69	73	14.5	542	2	Q8GYA1
70	73	14.5	584	2	Q9AAR5
71	73	14.5	620	1	DXS_BORBR
72	73	14.5	620	1	DXS_BORPE
73	73	14.5	630	1	DXS_BORPE
74	73	14.5	802	2	Q6F5A9
75	73	14.5	802	2	Q6C383
76	73	14.5	1279	2	Q46099
77	73	14.5	1552	2	Q67SX8
78	73	14.4	240	2	Q84CV5
79	72.5	14.4	373	2	Q7YWC1
80	72.5	14.4	384	2	Q88KE1
81	72.5	14.4	421	2	Q93177
82	72.5	14.4	421	2	Q72KV7
83	72.5	14.4	482	2	Q9BHF9
84	72.5	14.4	616	2	Q7W2M5
85	72.5	14.4	3165	2	Q939Z1
86	72	14.3	236	2	Q26351
87	72	14.3	397	1	SUCC_AGR15
88	72	14.3	413	2	Q98NR3
89	72	14.3	438	2	Q744A8
90	72	14.3	518	2	Q7D6T0
91	72	14.3	528	2	P71969
92	72	14.3	528	2	Q7TW52
93	72	14.3	531	2	Q9RJ14
94	72	14.3	589	2	Q6CJZ1
95	71.5	14.2	88	2	Q6A4X0
96	71.5	14.2	343	2	Q88WU3
97	71.5	14.2	460	2	Q749Y1
98	71.5	14.2	462	2	Q9A3U4
99	71.5	14.2	474	2	Q89FZ0
100	71.5	14.2	520	2	Q94E69
101	71.5	14.2	590	2	Q6LT07
102	71.5	14.2	694	2	Q8KBL2
103	71.5	14.2	874	1	CLPB_AGR15
104	71	14.1	275	2	Q82U00
Q62IX9	burkholderi				
Q63SM0	burkholderi				
Q9ABL0	caulobacter				
Q32619	halicobacter				
Q8G4X4	bifidobacte				
Q9F2I6	streptomyce				
Q8G3S2	bifidobacte				
Q9YEG2	aeropyrum p				
Q8XRM8	raistonia b				
Q89XU3	bradyrhizob				
Q8RFX3	corynebacte				
Q9H16	homo sapien				
Q89H46	bradyrhizob				
Q8C313	mus musculu				
Q6FQW0	candida gla				
Q6N849	rhodospheud				
Q69UA9	oryza sativ				
Q75D55	ashbya gos				
Q6M849	corynebacte				
Q91OK1	streptomyce				
Q60670	mus musculu				
Q86D11	leishmania				
Q757F5	ashbya gos				
Q9HNI9	halobacteri				
Q8NQ28	corynebacte				
Q8EJ01	shewanella				
Q6AN39	desulfotale				
DXS_WIGBR	wisgilewort				
SNIL_RAT	oryza sativ				
SYA_THER2	rattus norv				
SYA_THER1	thermus the				
Q9GHB5	galleria me				
Q9BD48	rhizobium 1				
Q82SM1	streptomyce				
Q91512	pseudomonas				
Q6NHX3	corynebacte				
Q8GYA1	arabidopsis				
Q9AAR5	caulobacter				
DXS_BORBR	bordeletia				
DXS_BORPE	bordeletia				
Q6F5A9	xanthomonas				
Q6C383	xanthomonas				
Q46099	dirosophila				
Q67SX8	eymbiolacte				
Q84CV5	uncultured				
Q7YWC1	toxoplasma				
Q88KE1	pseudomonas				
Q93177	thermus the				
Q72KV7	thermus the				
Q9BHF9	leishmania				
Q7W2M5	bordeletia				
Q939Z1	amycolactops				
Q26351	leishmania				
SUCC_AGR15	agrobacteri				
Q98NR3	rhizobium 1				
Q744A8	mycobacteri				
Q7D6T0	mycobacteri				
P71969	mycobacteri				
Q7TW52	mycobacteri				
Q9RJ14	streptomyce				
Q6CJZ1	kluyveromyc				
Q6A4X0	malus domes				
Q88WU3	lactobacilli				
Q749Y1	geobacter s				
Q9A3U4	caulobacter				
Q89FZ0	bradyrhizob				
Q94E69	oryza sativ				
Q6LT07	photobacter				
Q8KBL2	chlorobium				
CLPB_AGR15	agrobacteri				
Q82U00	nitrosomonas				

105	71	14.1	315	2	Q89P63	Q89p63 bradyrhizob	178	69	13.7	865	1	CLPB_STRCO
106	71	14.1	322	2	Q85IR4	Q85ir4 oryza sativ	179	69	13.7	3295	2	Q74RT8
107	71	14.1	337	2	Q89TF3	Q89tf3 bradyrhizob	180	69	13.7	3295	2	Q82TA8
108	71	14.1	341	2	Q9AMX3	Q9amx3 bradyrhizob	181	69	13.7	3378	2	Q65S06
109	71	14.1	409	2	Q85SW5	Q85sw5 oryza sativ	182	68.5	13.6	202	2	Q92LS1
110	71	14.1	422	2	Q8ZUN5	Q8zun5 nitrosomona	183	68.5	13.6	208	2	Q7W2P8
111	71	14.1	428	1	FXB2_MOUSE	Q47f33 mus musculi	184	68.5	13.6	230	2	Q84CM2
112	71	14.1	440	2	Q91IO3	Q91i3 pseudomonas	185	68.5	13.6	248	2	Q7WDP6
113	71	14.1	448	2	Q826U4	Q826u4 streptomyces	186	68.5	13.6	277	2	Q7WDP6
114	71	14.1	480	2	Q826U4	Q826u4 streptomyces	187	68.5	13.6	281	2	Q8DJM7
115	71	14.1	721	1	DNA_RHIME	P35890 rhizobium m	188	68.5	13.6	302	2	Q8BPA3
116	71	14.1	721	2	Q73V99	Q73v99 mycobacteri	189	68.5	13.6	311	2	Q82CH3
117	71	14.1	826	2	Q74ER8	Q74er8 geobacteri	190	68.5	13.6	335	2	Q8ARF5
118	71	14.1	947	2	Q8FUF8	Q8ff8 bacterioidia	191	68.5	13.6	335	2	Q8ARF5
119	71	14.1	1541	2	Q63LO3	Q63l3 burkholderi	192	68.5	13.6	350	2	Q7CQZ9
120	70.5	14.0	260	2	Q93TA7	Q93ta7 mycobacteri	193	68.5	13.6	370	2	Q6N6I5
121	70.5	14.0	326	2	Q93EM4	Q93em4 desulfovibr	194	68.5	13.6	377	1	PROB_BIFLO
122	70.5	14.0	353	2	Q8XOV5	Q8xov5 avian ortho	195	68.5	13.6	391	2	Q6FER4
123	70.5	14.0	484	2	Q64H13	Q64hy3 mus musculi	196	68.5	13.6	402	2	Q8KNG9
124	70.5	14.0	668	2	Q23323	Q23323 arabidopsis	197	68.5	13.6	404	2	Q74I39
125	70.5	14.0	691	2	Q8FTB0	Q8ftb0 corynebacte	198	68.5	13.6	415	2	Q6AAB3
126	70.5	14.0	754	2	Q6ESB4	Q6esb4 oryza sativ	199	68.5	13.6	434	2	Q73V12
127	70.5	14.0	830	2	Q6ESB5	Q6esb5 oryza sativ	200	68.5	13.6	499	2	Q82M67
128	70.5	14.0	937	2	Q6N973	Q6n973 rhodospheo	201	68.5	13.6	507	2	Q829B3
129	70	13.9	122	2	Q63RP5	Q63rf5 burkholderi	202	68.5	13.6	541	2	Q985J3
130	70	13.9	135	2	Q33526	Q33526 rhizobium l	203	68.5	13.6	556	2	Q6GK21
131	70	13.9	334	2	Q98B15	Q98b15 rhizobium l	204	68.5	13.6	774	2	P95636
132	70	13.9	403	2	Q88911	Q88911 pseudomonas	205	68.5	13.6	777	2	Q6NCO4
133	70	13.9	436	2	Q8FWQ3	Q8fwq3 brucella su	206	68.5	13.6	1267	2	Q9UUD5
134	70	13.9	407	1	SUFS_ERWCT	Q64625 erwina car	207	68.5	13.6	1724	2	Q25425
135	70	13.9	425	2	Q6CTJ9	Q6ctj9 yarrowia l1	208	68	13.5	118	2	Q9SMN1
136	70	13.9	431	2	Q23028	Q23028 arabidopsis	209	68	13.5	126	2	Q6NJC5
137	70	13.9	452	2	Q82N06	Q82n06 streptomyce	210	68	13.5	184	2	Q6FZP1
138	70	13.9	466	2	Q82N06	Q82n06 streptomyce	211	68	13.5	202	2	Q6ESZ8
139	70	13.9	477	2	Q9KHN5	Q9khn5 vibrio chol	212	68	13.5	221	2	Q62T59
140	70	13.9	491	2	Q89VK1	Q89vk1 bradyrhizob	213	68	13.5	266	2	Q92TR1
141	70	13.9	632	2	Q89VK1	Q89vk1 mycobacteri	214	68	13.5	308	2	Q6A5B8
142	70	13.9	689	2	Q98EK7	Q98ek7 rhizobium l	215	68	13.5	331	2	Q6AB84
143	70	13.9	88	2	Q98EK7	Q98ek7 rhizobium l	216	68	13.5	334	1	FEPP_ECOLI
144	69.5	13.8	102	2	Q98EK7	Q98ek7 leishmania	217	68	13.5	334	2	Q8XBV5
145	69.5	13.8	244	2	P74128	P74128 synecocyst	218	68	13.5	338	2	Q8FK21
146	69.5	13.8	305	2	Q8BM41	Q8bm41 mus muscu	219	68	13.5	338	2	Q83SB7
147	69.5	13.8	362	2	Q88OE2	Q88oe2 pseudomonas	220	68	13.5	360	2	Q91UX1
148	69.5	13.8	387	2	Q88OE2	Q88oe2 pseudomonas	221	68	13.5	377	2	Q9FRT6
149	69.5	13.8	396	2	Q9VR22	Q9vr22 deinococcus	222	68	13.5	407	2	Q67BA4
150	69.5	13.8	409	2	Q8Y2W6	Q8y2w6 ralstonia s	223	68	13.5	456	2	Q91CWO
151	69.5	13.8	423	2	Q79FV1	Q79fv1 mycobacteri	224	68	13.5	560	2	Q86320
152	69.5	13.8	423	2	Q79FV1	Q79fv1 mycobacteri	225	68	13.5	560	2	Q7WVC1
153	69.5	13.8	426	2	Q7D938	Q7d938 mycobacteri	226	68	13.5	569	1	SILF_MOUSE
154	69.5	13.8	426	2	Q7D938	Q7d938 mycobacteri	227	68	13.5	584	2	Q7W6E4
155	69.5	13.8	427	2	Q9FB37	Q9fb37 streptomyce	228	68	13.5	589	2	Q7W6F3
156	69.5	13.8	455	2	Q82599	Q82599 salmoneila	229	68	13.5	618	2	Q6A6E0
157	69.5	13.8	455	2	Q82599	Q82599 salmoneila	230	68	13.5	659	2	Q7W6Y5
158	69.5	13.8	495	2	Q82N13	Q82n13 salmoneila	231	68	13.5	1243	2	Q84HK8
159	69.5	13.8	567	2	Q98M48	Q98m48 rhizobium l	232	68	13.5	1243	2	Q6WPM3
160	69.5	13.8	583	2	Q98M48	Q98m48 rhizobium l	233	68	13.5	1243	2	Q6WPM3
161	69.5	13.8	636	2	Q89S07	Q89s07 bradyrhizob	234	68	13.5	168	2	Q69ML9
162	69.5	13.8	650	2	Q65IK5	Q65ik5 oryza sativ	235	67.5	13.4	227	2	Q69ML9
163	69.5	13.8	723	2	Q65IK5	Q65ik5 oryza sativ	236	67.5	13.4	253	2	Q69ML9
164	69.5	13.8	723	2	Q65IK5	Q65ik5 oryza sativ	237	67.5	13.4	253	2	Q69ML9
165	69.5	13.8	1419	2	Q6AMW5	Q6amw5 debaromyce	238	67.5	13.4	266	2	Q93US2
166	69.5	13.8	1427	2	Q6CZ75	Q6cz75 erwina car	239	67.5	13.4	292	2	Q7W5E3
167	69	13.7	124	1	RL7_RALISO	Q8xuz7 ralstonia s	240	67.5	13.4	306	2	Q88V34
168	69	13.7	141	2	Q7NHU5	Q7nhu5 ralstonia s	241	67.5	13.4	312	2	Q7W0A1
169	69	13.7	170	2	Q8YIC0	Q8yic0 brucella me	242	67.5	13.4	342	2	Q889K2
170	69	13.7	285	2	Q6CR99	Q6cr99 kluyveromyc	243	67.5	13.4	343	2	Q7W1P6
171	69	13.7	353	2	Q72GNS	Q72gns thermus the	244	67.5	13.4	349	2	Q92V91
172	69	13.7	359	2	Q72GNS	Q72gns thermus the	245	67.5	13.4	367	2	Q7T2B9
173	69	13.7	388	2	Q7W447	Q7w447 rhodopirell	246	67.5	13.4	367	2	Q8H6B8
174	69	13.7	512	2	Q7WPE6	Q7wpe6 bradyrhizob	247	67.5	13.4	387	2	Q7WNP3
175	69	13.7	541	2	Q89E27	Q89e27 ralstonia s	248	67.5	13.4	387	2	Q9RSK2
176	69	13.7	581	2	Q8XOV8	Q8xov8 ralstonia s	249	67.5	13.4	408	2	Q72C12
177	69	13.7	627	2	Q9RUD0	Q9rud0 deinococcus	250	67.5	13.4			

251	67.5	13.4	470	2	Q6AB56	Q6ab6 propionibac	324	66.5	13.2	446	2	Q6D7N9	Q6d7n9 erwinia car
252	67.5	13.4	491	2	Q9J396	Q9j396 streptomyce	325	66.5	13.2	448	2	Q8TKX9	Q8tkx9 methanosarc
253	67.5	13.4	520	2	Q8ABF7	Q8abf7 bacteroides	326	66.5	13.2	465	1	FXDI_HUMAN	O16676 homo sapien
254	67.5	13.4	571	2	Q75R19	Q75e19 ashyia goss	327	66.5	13.2	491	2	Q9PG00	Q9fg00 arabidopsis
255	67.5	13.4	583	2	Q82B40	Q82b40 streptomyce	328	66.5	13.2	502	2	Q6E0R8	Q6e0r8 borrelia ga
256	67.5	13.4	588	2	Q7NH19	Q7nh19 gloeobacter	329	66.5	13.2	502	2	Q82K76	Q82k76 streptomyce
257	67.5	13.4	603	2	Q8FPU0	Q8fpu0 corynebacte	330	66.5	13.2	545	2	Q7X7G3	Q7xcg3 oryza sativ
258	67.5	13.4	782	2	Q6YUW7	Q6yuw7 oryza sativ	331	66.5	13.2	587	2	Q65Z17	Q65z17 chlamydomon
259	67.5	13.4	784	2	Q50199	Q50199 mycobacteri	332	66.5	13.2	667	2	Q938J9	Q938j9 caenorhabdt
260	67.5	13.4	942	2	Q8CAH0	Q8cah0 mus musculu	333	66.5	13.2	752	2	Q8FWM1	Q8fm11 corynebacte
261	67.5	13.4	1179	2	Q87E19	Q87e19 xylella fas	334	66.5	13.2	838	2	Q6ACL7	Q6acl7 leishonia x
262	67.5	13.4	1179	2	Q9PD26	Q9pd26 xylella fas	335	66.5	13.2	873	1	E74H_DROVI	Q7m36 dirosophila
263	67.5	13.4	1206	2	Q9CCX9	Q9ccx9 mycobacteri	336	66.5	13.2	1114	2	Q8A7H2	Q8a7h2 bacteroides
264	67.5	13.4	1245	2	Q9RL54	Q9rl54 streptomyce	337	66.5	13.2	1510	2	Q80179	Q80179 streptococc
265	67.5	13.4	1389	2	Q6MG27	Q6mg27 mycobacteri	338	66.5	13.2	1787	2	Q9MAX9	Q9max9 chlamydomon
266	67.5	13.4	1452	2	Q6MG26	Q6mg26 mycobacteri	339	66.5	13.2	2006	2	Q8XCE7	Q8xc7 raleronia s
267	67.5	13.4	1840	2	Q6PDI5	Q6pdi5 mus musculu	340	66.5	13.2	2737	2	Q8XPU7	Q8xpu7 ralsstonia s
268	67.5	13.4	2035	1	F38A_HUMAN	Q92508 homo sapien	341	66.5	13.2	2948	2	Q86WG6	Q86wg6 homo sapien
269	67.5	13.4	2698	2	Q9XIR5	Q9xir5 arabidopsis	342	66.5	13.2	3288	2	Q7T5D9	Q7t5d9 cercoplithec
270	67.5	13.4	14130	2	Q6MZ72	Q6mz72 mycobacteri	343	66.5	13.2	3326	2	Q7T591	Q7t591 cercoplithec
271	67.5	13.4	16990	2	Q6MZA4	Q6mza4 mycobacteri	344	66	13.1	103	2	Q9KJ37	Q9kj37 leprolyngby
272	67	13.3	109	2	Q9VY10	Q9vy10 dirosophila	345	66	13.1	118	1	NLTD_BRAOL	Q43304 brasica o1
273	67	13.3	147	2	Q9AF35	Q9af35 uncultured	346	66	13.1	121	1	MP70_MYCKA	Q49614 mycobacteri
274	67	13.3	147	2	Q8PEB1	Q8pei1 xanthomonas	347	66	13.1	239	1	CLRC_IDBDE	Q60000 ideonella d
275	67	13.3	218	2	Q9KSI6	Q9ksi6 vibrio chol	348	66	13.1	266	2	Q83Y03	Q83y03 uncultured
276	67	13.3	228	2	Q9UY11	Q9uy11 pyrococcus	349	66	13.1	293	2	Q7NLV1	Q7nlv1 gloeobacter
277	67	13.3	243	2	Q8YV28	Q8yv28 bradyrhizob	350	66	13.1	306	2	Q7JSE1	Q7jse1 mycobacteri
278	67	13.3	297	2	Q6N709	Q6n709 rhodopseudo	351	66	13.1	310	2	Q668Z9	Q668z9 yerastinia ps
279	67	13.3	346	2	Q8KR73	Q8kr73 photorhabdu	352	66	13.1	310	2	Q8ZDK6	Q8zdk6 yerastinia pe
280	67	13.3	351	1	GCP_MYCLE	Q8kr73 mycobacteri	353	66	13.1	314	2	Q74R26	Q74r26 yerastinia pe
281	67	13.3	368	2	Q92RF4	Q92rf4 rhizobium m	354	66	13.1	329	2	Q7NJ15	Q7nj15 gloeobacter
282	67	13.3	369	2	Q6SLP3	Q6slp3 oryza sativ	355	66	13.1	330	2	Q9KP40	Q9kp40 vibrio chol
283	67	13.3	419	2	Q8YBM4	Q8ybm4 bruceella me	356	66	13.1	331	2	Q8RGF4	Q8rgf4 fusobacteri
284	67	13.3	444	1	FUMC_PBSM	Q8b5v0 pseudomonas	357	66	13.1	335	2	Q8FTH0	Q8ft0 corynebacte
285	67	13.3	472	2	Q8PHB8	Q8phb8 xanthomonas	358	66	13.1	337	2	Q9K6G3	Q9k6g3 bacillus ha
286	67	13.3	487	2	Q9EY49	Q9ey49 pseudomonas	359	66	13.1	373	2	Q63NQ9	Q63nq9 burkholderi
287	67	13.3	636	2	Q9EY10	Q9ey10 aeropyrum p	360	66	13.1	396	2	Q82QW0	Q82qw0 streptomyce
288	67	13.3	724	2	Q9ABE7	Q9abe7 caulobacter	361	66	13.1	400	2	Q8U488	Q8u488 pyrococcus
289	67	13.3	746	2	Q7OR12	Q7orf2 anopheles g	362	66	13.1	409	2	Q9BG71	Q9bg71 rhizobium 1
290	67	13.3	760	2	Q8FRU0	Q8fru0 anabeana sp	363	66	13.1	442	2	Q6DOL4	Q6dol4 erwinia car
291	67	13.3	772	2	Q7Q6Z6	Q7q6z6 anopheles g	364	66	13.1	448	1	PLSX_PROMM	Q7v477 prochlororoc
292	67	13.3	840	2	Q9A7G5	Q9a7g5 caulobacter	365	66	13.1	456	2	Q7MTG2	Q7mtg2 streptomyce
293	67	13.3	848	2	Q7W1M4	Q7w1m4 bordetella	366	66	13.1	521	2	Q7SCZ8	Q7scz8 neurospora
294	67	13.3	854	1	CLPB_PSRPK	Q88g71 pseudomonas	367	66	13.1	527	1	PTB_MOUSE	Q7ec28 mus musculu
295	67	13.3	856	2	Q65RMO	Q65rmo manhelina	368	66	13.1	529	2	Q6AAL8	Q6aal8 propionibac
296	67	13.3	1041	2	Q8CKO5	Q8cko5 streptomyce	369	66	13.1	538	2	Q6ISK7	Q6isk7 oryza sativ
297	67	13.3	1249	2	Q9BKX3	Q9bkx3 homo sapien	370	66	13.1	540	1	LEU1_PROMM	Q7tuv5 prochlororoc
298	67	13.3	1747	2	Q9NBQ1	Q9nbq1 trypanosoma	371	66	13.1	581	2	Q6V7G5	Q6v7g5 vibrio para
299	67	13.3	2541	2	Q8AM10	Q8am10 gallus gall	372	66	13.1	581	2	Q986R2	Q986r2 rhizobium 1
300	67	13.3	13536	2	Q83VS0	Q83vs0 pseudomonas	373	66	13.1	585	1	NUP1_RAT	P70581 ratus norv
301	66.5	13.2	106	2	Q9Z7V3	Q9z7v3 chlamydia p	374	66	13.1	603	2	Q7QBL4	Q7qbl4 anopheles g
302	66.5	13.2	112	2	Q6IED3	Q6ied3 bos taurus	375	66	13.1	613	2	Q8ZBL8	Q8zbl8 streptomyce
303	66.5	13.2	144	2	Q70KA2	Q70ka2 gordonia we	376	66	13.1	638	2	Q41768	Q41768 zea mays (m
304	66.5	13.2	146	2	Q9YD19	Q9ydl9 aeropyrum p	377	66	13.1	665	2	Q9F5F6	Q9f5f6 agrobacteri
305	66.5	13.2	172	2	Q7U521	Q7u521 synechococc	378	66	13.1	686	2	Q82V51	Q82v51 nitrosomona
306	66.5	13.2	178	2	Q946W0	Q946w0 zea mays (m	379	66	13.1	697	2	Q745I8	Q745i8 mycobacteri
307	66.5	13.2	180	2	Q41888	Q41888 zea mays (m	380	66	13.1	710	2	Q7WEC6	Q7wec6 bordetella
308	66.5	13.2	195	2	Q7XRX4	Q7xrx4 oryza sativ	381	66	13.1	817	2	Q964V6	Q964v6 dictyostell
309	66.5	13.2	243	2	Q88062	Q88062 streptomyce	382	66	13.1	823	2	Q9B0J9	Q9b0j9 mycobacteri
310	66.5	13.2	245	2	Q89GZ5	Q89gz5 bradyrhizob	383	66	13.1	857	1	CLPB_STRAL	Q9z664 streptomyce
311	66.5	13.2	291	2	Q84FP5	Q84fp5 apitullina p	384	66	13.1	879	1	CLPB_BRAVA	Q89u12 bradyrhizob
312	66.5	13.2	304	2	Q8KX52	Q8kx52 uncultured	385	66	13.1	934	2	Q6C2T4	Q6c2t4 yarrowia 11
313	66.5	13.2	307	2	Q74HB8	Q74hb8 lactobacill	386	66	13.1	999	2	Q7P102	Q7p102 chromobacte
314	66.5	13.2	322	2	Q88918	Q88918 pseudomonas	387	66	13.1	1043	2	Q85157	Q85157 photorhabdu
315	66.5	13.2	326	2	Q7W4P0	Q7w4p0 bordetella	388	66	13.1	1366	2	Q8K7N9	Q8k7n9 streptococc
316	66.5	13.2	336	2	Q7MG66	Q7mg66 bordetella	389	66	13.1	1372	2	Q878N3	Q878n3 streptococc
317	66.5	13.2	333	2	Q8PI08	Q8pi08 xanthomonas	390	66	13.1	1400	2	Q7DA75	Q7das7 mycobacteri
318	66.5	13.2	341	1	TA2R_RAT	B34978 ratus norv	391	66	13.1	1400	2	P964J9	P964j9 mycobacteri
319	66.5	13.2	368	2	Q8GFF1	Q8gff1 streptomyce	392	66	13.1	1400	2	Q7U2H8	Q7u2h8 mycobacteri
320	66.5	13.2	377	2	Q6E208	Q6e208 edwardsiell	393	66	13.1	1467	2	Q9K175	Q9k175 nitrococcus
321	66.5	13.2	377	2	Q82N80	Q82n80 streptomyce	394	66	13.1	1654	2	Q7KR59	Q7kr59 dirosophila
322	66.5	13.2	389	2	Q986N1	Q986n1 rhizobium 1	395	66	13.1	1674	2	Q9V9V5	Q9v9v5 dirosophila
323	66.5	13.2	437	2	Q9AMU5	Q9amu5 bradyrhizob	396	65.5	13.0	122	2	Q81249	Q81249 salmonella

397	65.5	13.0	183	2	08PA47	08p47 xanthomonas	470	65	12.9	312	2	09H227	09h27 pseudomonas
398	65.5	13.0	212	2	06SV37	06sv37 mantheimia	471	65	12.9	331	2	07WK72	07wk72 bordetella
399	65.5	13.0	226	2	093MT8	093mt8 uncultured	472	65	12.9	344	1	TRD2_RALSO	08x60 ralstonia s
400	65.5	13.0	257	1	EUTC_RHOER	059782 rhodococcus	473	65	12.9	350	2	06W1MO	06w1mo rhizobium s
401	65.5	13.0	254	2	09A6M8	09a6m8 caulobacter	474	65	12.9	358	1	CHB2_PSESM	08b8v8 pseudomonas
402	65.5	13.0	266	2	093UR8	093ur8 desulfocvbr	475	65	12.9	367	2	08YAV1	08yav1 brucella me
403	65.5	13.0	289	2	056024	056024 salmoneilla	476	65	12.9	367	2	08FXG2	08fxg2 brucella su
404	65.5	13.0	321	2	0839P4	0839p4 enterococcu	477	65	12.9	368	2	07ZE12	07ze12 desulfocvbr
405	65.5	13.0	326	2	08R532	08r532 mus musculu	478	65	12.9	370	2	07WM49	07wm49 bordetella
406	65.5	13.0	335	2	089MP4	089mp4 bradyrhizob	479	65	12.9	370	2	07WEK7	07wek7 bordetella
407	65.5	13.0	336	1	COER_RHILLO	089mp4 bradyrhizob	480	65	12.9	370	2	07MD43	07md43 bordetella
408	65.5	13.0	343	2	09L3J4	09lp34 arabidopsis	481	65	12.9	385	2	08V0Z0	08v0z0 mycobacteri
409	65.5	13.0	344	2	08GVF7	08gvf7 oryza sativ	482	65	12.9	385	2	07ZEL6	07zel6 mycobacteri
410	65.5	13.0	361	2	092S90	092s90 rhizobium m	483	65	12.9	385	2	07TZR7	07tzt7 mycobacteri
411	65.5	13.0	361	2	09A2C3	09a2c3 caulobacter	484	65	12.9	391	2	08XY45	08xy45 ralstonia s
412	65.5	13.0	383	2	06ZPS4	06zps4 burkholderi	485	65	12.9	393	2	08XK05	08xk05 streptococc
413	65.5	13.0	383	2	063PH2	063ph2 burkholderi	486	65	12.9	399	1	YMG6_SYNEL	08gmu0 synecchococ
414	65.5	13.0	393	2	098L25	098l25 rhizobium 1	487	65	12.9	410	2	073Y22	073y22 mycobacteri
415	65.5	13.0	402	2	07Z7Q2	07z7q2 homo sapien	488	65	12.9	416	2	073Y22	073y22 mycobacteri
416	65.5	13.0	436	2	099PE1	099pe1 mus musculu	489	65	12.9	426	2	093JG9	093jg9 streptococc
417	65.5	13.0	455	2	082L73	082l73 streptomyce	490	65	12.9	427	2	09RLJ0	09rlj0 pseudomonas
418	65.5	13.0	457	2	094DES	094des oryza sativ	491	65	12.9	427	2	ARGJ_PROMM	07v436 p arginine
419	65.5	13.0	470	2	073VU4	073vu4 mycobacteri	492	65	12.9	429	2	08N835	08n835 rhodopseudo
420	65.5	13.0	491	2	YOB4_MYCTU	053209 mycobacteri	493	65	12.9	442	1	09LS41	09ls41 ataxidopais
421	65.5	13.0	491	2	07TVH3	07tvh3 mycobacteri	494	65	12.9	462	2	A2NC_HUMAN	08ra13 thiermaner
422	65.5	13.0	535	2	07WMU4	07wm4 pseudomonas	495	65	12.9	462	2	072C38	072c38 homo sapien
423	65.5	13.0	539	2	087WC7	087wc7 pseudomonas	496	65	12.9	482	2	06EYF4	06eyf4 cyprinodon
424	65.5	13.0	556	2	08CK61	08ck61 erwinia car	497	65	12.9	525	2	08B4G0	08b4g0 desulfocvbr
425	65.5	13.0	564	2	08CK61	08ck61 streptomyce	498	65	12.9	544	2	06T442	06t442 rhizobium 1
426	65.5	13.0	593	2	079BT1	079bt1 salmoneilla	499	65	12.9	603	2	06VT01	06vt01 leishmania
427	65.5	13.0	593	2	056114	056114 salmoneilla	500	65	12.9	617	2	06UYF6	06uyf6 vibrio para
428	65.5	13.0	593	2	056114	056114 salmoneilla	501	65	12.9	617	2	06UKA7	06uka7 burkholderi
429	65.5	13.0	616	2	07VSP8	07vst8 bordetella	502	65	12.9	631	2	08HAU7	08ha17 burkholderi
430	65.5	13.0	616	2	07WDM1	07wdm1 bordetella	503	65	12.9	680	2	08NVN4	08nv4 bradyrhizob
431	65.5	13.0	618	2	093JH7	093jh7 streptomyce	504	65	12.9	680	2	08E027	08e027 mycoplasma
432	65.5	13.0	631	2	092K91	092k91 rhizobium m	505	65	12.9	680	2	RECG_ECOLI	09kh14 escherichia
433	65.5	13.0	635	2	06L0G9	06l0g9 photobacter	506	65	12.9	693	1	08XK14	08xk14 escherichia
434	65.5	13.0	658	2	06R8C5	06r8c5 sedalia glo	507	65	12.9	693	1	07UB01	07ub01 shigella fl
435	65.5	13.0	665	2	07P987	07p987 rickettsia	508	65	12.9	704	2	0821A1	0821a1 escherichia
436	65.5	13.0	665	2	092H13	092h13 rickettsia	509	65	12.9	704	2	08FC81	08fc81 rhodospirill
437	65.5	13.0	682	2	09NKA3	09nka3 homo sapien	510	65	12.9	706	2	07X4W5	07x4w5 rhodospirill
438	65.5	13.0	713	2	084NK5	084nk5 oryza sativ	511	65	12.9	771	2	0629Y1	0629y1 burkholderi
439	65.5	13.0	803	2	093H85	093h85 bradyrhizob	512	65	12.9	771	2	063123	063123 burkholderi
440	65.5	13.0	808	2	07VV44	07vv44 bordetella	513	65	12.9	786	2	08S053	08s053 oryza sativ
441	65.5	13.0	808	2	07VW60	07vw60 bordetella	514	65	12.9	845	2	09UPP0	09upp0 homo sapien
442	65.5	13.0	846	1	CLPB_MYCLE	06vg29 pseudomonas	515	65	12.9	857	2	06A678	06a678 propionibac
443	65.5	13.0	848	1	CLPB_XYLFA	09p26 mycobacteri	516	65	12.9	910	2	060324	060324 homo sapien
444	65.5	13.0	861	1	CLPB_XYLFA	09p26 mycobacteri	517	65	12.9	949	2	08W7Q9	08w7q9 homo sapien
445	65.5	13.0	861	1	CLPB_XYLFA	09p26 mycobacteri	518	65	12.9	1024	2	077CD5	077cd5 bovine hepr
446	65.5	13.0	863	2	06HND3	06hnd3 rattus norv	519	65	12.9	1024	2	06Y3H7	06y3h7 chlamydomon
447	65.5	13.0	879	1	CLPB_RHOPA	09jmd2 rattus norv	520	65	12.9	1024	2	06Y3H7	06y3h7 chlamydomon
448	65.5	13.0	898	1	0823I9	0823i9 chlamydomon	521	65	12.9	1892	2	084HM3	084hm3 neosporea
449	65.5	13.0	1246	2	09Y632	09y632 homo sapien	522	65	12.9	2092	2	07SA55	07sa55 neosporea
450	65.5	13.0	1685	2	09UM8	09um8 homo sapien	523	65	12.9	2632	2	070511	070511 rattus norv
451	65.5	13.0	2303	2	09S596	09s596 homo sapien	524	65	12.9	2849	2	08W6K4	08w6k4 simonrhizob
452	65.5	13.0	2601	2	08XPU1	08xpu1 ralstonia s	525	65	12.9	4106	2	0846X2	0846x2 streptomyce
453	65.5	13.0	4928	2	09ALM3	09alm3 saccharopol	526	65	12.9	4377	1	ANK3_HUMAN	012955 homo sapien
454	65	12.9	88	2	067L12	067l12 symbiobacte	527	65	12.9	5216	2	09VXZ5	09vxz5 drosophila
455	65	12.9	126	2	063N39	063n39 burkholderi	528	65	12.9	5233	2	09NB71	09nb71 drosophila
456	65	12.9	147	2	07X9S9	07x9s9 burkholderi	529	65	12.9	89	2	041378	041378 benecio odo
457	65	12.9	148	2	09AR34	09ar34 uncultured	530	65	12.9	184	1	CYCM_BAATA	041378 benecio odo
458	65	12.9	219	2	08P8U4	08p8u4 xanthomonas	531	65	12.9	189	2	08A8L9	08a8l9 bradyrhizob
459	65	12.9	219	2	08P8U4	08p8u4 xanthomonas	532	65	12.9	214	2	08A8L9	08a8l9 bacteroides
460	65	12.9	236	2	06RKH5	06rkus xanthomonas	533	65	12.9	245	2	082A87	082a87 streptomyce
461	65	12.9	236	2	06RKH5	06rkus xanthomonas	534	65	12.9	245	2	07W6X0	07w6x0 bordetella
462	65	12.9	238	2	0745R3	0745r3 mycobacteri	535	65	12.9	257	2	07XST9	07xst9 oryza sativ
463	65	12.9	261	2	086977	086977 desulfococ	536	65	12.9	294	2	08XZ47	08xz47 pyrobaculum
464	65	12.9	267	2	08NMS9	08nms9 uncultured	537	65	12.9	320	1	Y678_METUA	08xat1 pyrobaculum
465	65	12.9	267	2	09A346	09a346 caulobacter	538	65	12.9	321	2	08CNG5	08cng5 stephyllococ
466	65	12.9	275	2	0918X0	0918x0 aeropyrum p	539	65	12.9	328	2	08G6X1	08g6x1 gallus galli
467	65	12.9	276	2	065599	065599 arabidopsis	540	65	12.9	331	2	08VYEO	08vyeo brucella su
468	65	12.9	281	2	09XCV3	09xcv3 flavobacter	541	65	12.9	337	2	08VYEO	08vyeo brucella su
469	65	12.9	300	2	072K11	072k11 thermus the	542	65	12.9	346	2	09A903	09a903 caulobacter

543	64.5	12.8	363	2	Q89H39	Q89h39 bradyrhizob	616	64	12.7	327	1	TH14 ASPOR	Q9unz9 aspergillus
544	64.5	12.8	366	2	Q8FM30	Q8fm30 corynebacte	617	64	12.7	339	2	Q8R3J0	Q8r3j0 mus musculu
545	64.5	12.8	375	2	Q7WwM0	Q7waw0 bordetella	618	64	12.7	345	2	Q8SPB8	Q8spb8 glycine max
546	64.5	12.8	375	2	Q7WKL7	Q7wkl7 bordetella	619	64	12.7	392	2	Q44305	Q44305 acinetobact
547	64.5	12.8	375	2	Q9KZL8	Q9kzl8 streptomyce	620	64	12.7	400	2	Q8Z8H9	Q8zh9 streptomyc
548	64.5	12.8	378	2	Q749L4	Q749l4 geobacter s	621	64	12.7	409	2	Q8P9R8	Q8p9r8 xanthomonas
549	64.5	12.8	379	2	Q6NZ21	Q6nzz1 brachydanio	622	64	12.7	422	2	Q741X1	Q741x1 mycobacteri
550	64.5	12.8	379	2	Q72DP0	Q72dp0 desulfovibr	623	64	12.7	426	1	Y200 ANASP	Q8z08 anabena sp
551	64.5	12.8	384	2	Q6K9Y0	Q6k9y0 oryza sativ	624	64	12.7	426	2	Q7U9D6	Q7u9d6 synechococ
552	64.5	12.8	385	2	Q9HKM2	Q9hkm2 pseudomonas	625	64	12.7	437	2	Q7TXF8	Q7txf8 mycobacteri
553	64.5	12.8	390	2	Q6N1X1	Q6n1x1 rhodopseud	626	64	12.7	437	2	Q725H4	Q725h4 desulfovibr
554	64.5	12.8	411	2	Q9FAK7	Q9fak7 rhizobium 1	627	64	12.7	464	2	Q9JWX7	Q9jwx7 niseiselia m
555	64.5	12.8	411	2	Q9K646	Q9k646 bacillus ha	628	64	12.7	468	2	Q9FCB6	Q9fc6 streptomyc
556	64.5	12.8	412	2	Q9K3M1	Q9k3m1 streptomyc	629	64	12.7	469	2	Q9X803	Q9x83 streptomyc
557	64.5	12.8	431	2	Q8AR86	Q8ar86 oryza sativ	630	64	12.7	473	2	Q8Z7L5	Q8z7l5 streptomyc
558	64.5	12.8	433	2	Q8ZRP5	Q8zrp5 salmonella	631	64	12.7	487	1	DNA_AGR75	Q8ul1 agrobacteri
559	64.5	12.8	435	2	Q92LG6	Q92lg6 rhizobium m	632	64	12.7	490	2	Q7XHS0	Q7xhs0 oryza sativ
560	64.5	12.8	455	2	Q8JEW4	Q8jew4 coxiella bu	633	64	12.7	491	2	Q9PJG2	Q9pjg2 chlamydia m
561	64.5	12.8	461	2	Q63KJ1	Q63kj1 burholderi	634	64	12.7	501	2	Q9IBD0	Q9ibd0 brachydanio
562	64.5	12.8	463	2	Q88CP9	Q88cp9 pseudomonas	635	64	12.7	507	2	Q7PSJ7	Q7psj7 anopheles g
563	64.5	12.8	480	2	Q86704	Q86704 streptomyc	636	64	12.7	509	2	Q872L9	Q872l9 neuropept
564	64.5	12.8	482	2	Q9FAC7	Q9fac7 rhodococcus	637	64	12.7	516	2	Q8XSS2	Q8xss2 ralestonia s
565	64.5	12.8	486	2	Q6N2W0	Q6n2w0 rhodopseud	638	64	12.7	534	2	Q72WE4	Q72we4 brachydanio
566	64.5	12.8	512	2	Q8FWZ4	Q8fwz4 bruceella su	639	64	12.7	537	2	Q8FQM7	Q8fqm7 corynebacte
567	64.5	12.8	529	2	Q9KMV5	Q9kmv5 vibrio chol	640	64	12.7	569	2	Q9RUJ3	Q9ruj3 deinococcus
568	64.5	12.8	559	2	Q8FTL2	Q8ftl2 corynebacte	641	64	12.7	582	2	Q72DM1	Q72dm1 desulfovibr
569	64.5	12.8	567	2	Q98ET7	Q98et7 rhizobium 1	642	64	12.7	600	2	Q8UJ21	Q8uj21 oryzae lat
570	64.5	12.8	619	2	Q67RS7	Q67rs7 symbiobacte	643	64	12.7	604	2	Q7WED8	Q7wed8 bordetella
571	64.5	12.8	629	2	Q751E0	Q75le0 abhya goss	644	64	12.7	607	2	Q7V632	Q7v632 bordetella
572	64.5	12.8	668	2	Q6ADN3	Q6apn3 desulfocale	645	64	12.7	618	2	Q6BP23	Q6bp23 oryza sativ
573	64.5	12.8	669	2	Q6A8G5	Q6a8g5 propionibac	646	64	12.7	637	2	Q9AAK8	Q9aak8 caulobacter
574	64.5	12.8	688	2	Q6MWC1	Q6mwc1 bdellovibr	647	64	12.7	655	1	YAGF_ECOLI	P7596 escherichia
575	64.5	12.8	780	1	ELS_CHICK	P07916 gallus gall	648	64	12.7	693	1	REC8_ECO57	Q8x86 escherichia
576	64.5	12.8	752	2	Q9K4U6	Q9k4u6 streptomyc	649	64	12.7	698	2	Q9A537	Q9a537 caulobacter
577	64.5	12.8	861	1	CLPB_XYLFT	Q87ax8 xyella fas	650	64	12.7	698	2	Q67KM1	Q67km1 symbiobacte
578	64.5	12.8	905	1	NUOG_PSEAB	Q91016 pseudomonas	651	64	12.7	700	2	Q6YXX1	Q6yxx1 oryza sativ
579	64.5	12.8	952	2	Q8X5G8	Q8x5g8 escherichia	652	64	12.7	702	2	Q89UV7	Q89uv7 bradyrhizob
580	64.5	12.8	1022	2	Q93MP2	Q93mp2 actinobacil	653	64	12.7	724	2	Q6FU10	Q6fu10 candida gla
581	64.5	12.8	1023	1	RT11_ACRPL	P55128 actinobacil	654	64	12.7	748	2	Q8CDI5	Q8cdi5 mus musculu
582	64.5	12.8	1023	1	RT12_ACPPL	P55129 actinobacil	655	64	12.7	790	2	Q9KM22	Q9km22 xanthomonas
583	64.5	12.8	1026	2	Q7ABP0	Q7aep0 escherichia	656	64	12.7	806	2	Q33967	Q33967 xanthomonas
584	64.5	12.8	1026	2	Q8XEJ2	Q8xej2 escherichia	657	64	12.7	813	2	Q7OKS2	Q7ok82 anopheles g
585	64.5	12.8	1030	2	Q7RZE3	Q7rze3 neurospora	658	64	12.7	926	2	Q8K287	Q8k287 mus musculu
586	64.5	12.8	1080	2	Q8XAH7	Q8xah7 escherichia	659	64	12.7	962	2	Q6KAU6	Q6kau6 mus musculu
587	64.5	12.8	1106	2	Q6XDB6	Q6xdb6 rattus norv	660	64	12.7	984	2	Q7QET1	Q7qet1 anopheles g
588	64.5	12.8	1159	1	RPOC_PORCN	Q33431 porphyromon	661	64	12.7	1043	2	Q7MZV7	Q7mzv7 photorhabdu
589	64.5	12.8	1161	2	Q9NEH0	Q9neh0 leishmania	662	64	12.7	1171	2	Q89DP3	Q89dp3 bradyrhizob
590	64.5	12.8	1240	2	Q9F3X7	Q9f3x7 porphyromon	663	64	12.7	1218	2	Q9F824	Q9fb24 streptomyc
591	64.5	12.8	1608	1	HLVA_SERMA	P15320 serratia ma	664	64	12.7	1303	2	Q9U172	Q9u172 leishmania
592	64.5	12.8	1608	2	Q8MOW4	Q8mqw4 drosochila	665	64	12.7	1480	2	Q8VWR0	Q8vwr0 photorhabdu
593	64.5	12.8	1767	2	Q80663	Q80663 aradidopsis	666	64	12.7	1480	2	Q7N9K8	Q7n9k8 photorhabdu
594	64.5	12.8	1910	2	Q7TZA7	Q7tza7 mycobacteri	667	64	12.7	1646	2	Q7WTE3	Q7wte3 streptomyc
595	64.5	12.8	2274	2	Q9ZIK7	Q9zlk7 mus musculu	668	64	12.7	2479	2	Q9A988	Q9a988 caulobacter
596	64.5	12.8	2404	2	Q9OBG4	Q9obg4 wheat yello	669	64	12.7	6842	2	Q84G24	Q84g24 streptomyc
597	64.5	12.8	2531	2	Q9VW47	Q9vw47 drosochila	670	64	12.6	82	1	C551_PSEME	P00102 pseudomonas
598	64.5	12.8	2541	1	TLN1_HUMAN	Q8y430 homo sapien	671	63.5	12.6	130	1	F14A_HUMAN	Q8h28 homo sapien
599	64.5	12.8	2541	2	Q86YD0	Q86y40 homo sapien	672	63.5	12.6	130	1	RL7_MYCLE	P30763 mycobacteri
600	64.5	12.8	2550	2	Q9UXP3	Q9upx3 homo sapien	673	63.5	12.6	147	2	Q7P0K6	Q7p0k6 chromobacte
601	64.5	12.8	7525	2	Q9KIE0	Q9kie0 streptomyc	674	63.5	12.6	172	2	Q6SK85	Q6sk85 arthrobacte
602	64	12.7	185	2	Q9RYJ5	Q9ryj5 deinococcus	675	63.5	12.6	173	2	Q9B206	Q9b206 calman croc
603	64	12.7	210	2	Q93969	Q93969 heterosigma	676	63.5	12.6	175	2	Q9YDF4	Q9ydf4 aeropyrum p
604	64	12.7	218	2	Q73W12	Q73w12 mycobacteri	677	63.5	12.6	198	2	Q7NNM7	Q7nnm7 gloeobacter
605	64	12.7	226	2	Q88AV1	Q88av1 pseudomonas	678	63.5	12.6	218	2	Q61BD4	Q61bd4 bos taurus
606	64	12.7	246	1	HIS4_METMA	Q8pw2 methanosarc	679	63.5	12.6	218	2	Q6ZFN1	Q6zfn1 oryza sativ
607	64	12.7	247	2	Q848N3	Q848n3 uncultured	680	63.5	12.6	225	2	Q888S7	Q888s7 pseudomonas
608	64	12.7	249	2	Q84ZM7	Q84zm7 oryza sativ	681	63.5	12.6	230	1	FLGH_XANCP	Q8p99 xanthomonas
609	64	12.7	261	2	Q54990	Q54990 streptomyc	682	63.5	12.6	248	2	Q7RZW8	Q7rzw8 neurospora
610	64	12.7	284	2	Q67J88	Q67j88 symbiobacte	683	63.5	12.6	252	2	Q7XTN9	Q7xtn9 oryza sativ
611	64	12.7	305	2	Q89H38	Q89h38 bradyrhizob	684	63.5	12.6	263	1	ZUP1_CORGL	Q8ngk0 corynebacto
612	64	12.7	308	2	Q8XUD0	Q8xud0 ralestonia s	685	63.5	12.6	263	2	Q05919	Q05919 mycobacteri
613	64	12.7	313	2	Q7YZX5	Q7yzx5 trypanosoma	686	63.5	12.6	263	2	Q7U104	Q7u104 mycobacteri
614	64	12.7	321	2	Q7W1L9	Q7w1l9 bordetella	687	63.5	12.6	264	2	Q6ADW8	Q6adw8 leifsonia x
615	64	12.7	321	2	Q7WPL0	Q7wpl0 bordetella	688	63.5	12.6	269	2	Q7W6M3	Q7w6m3 wolfinella s

835	63	12.5	470	2	Q7X4G1	Q7X4G1 xanthomonas	908	62.5	12.5	297	2	Q7NW70	Q7nw70 chromobacter
836	63	12.5	489	2	Q9DBE7	Q9dbef m mus muscu	909	62.5	12.5	299	2	Q7VTP0	Q7vtp0 bordetella
837	63	12.5	489	2	Q9ESV8	Q9esv8 rattus norv	910	62.5	12.5	304	2	Q7MTL0	Q7mtl0 porphyromon
838	63	12.5	495	2	Q9ET50	Q9et50 rattus norv	911	62.5	12.5	307	2	Q8GTL1	Q8gtl1 synechococ
839	63	12.5	505	2	Q9SQK4	Q9sqk4 vitis vinif	912	62.5	12.5	307	2	Q82PU2	Q82pu2 streptomyce
840	63	12.5	517	1	6PGD CANAL	013287 candida alb	913	62.5	12.5	314	2	Q75PX9	Q75px9 serratia ma
841	63	12.5	532	2	Q8K4G2	Q8k4g2 mus musculu	914	62.5	12.5	314	2	Q9A8B8	Q9a8b8 caulobacter
842	63	12.5	532	2	Q406G2	Q406g2 human papil	915	62.5	12.5	330	2	Q67P82	Q67p82 symbiobacter
843	63	12.5	540	2	Q87AC8	Q87ac8 xyloella fas	916	62.5	12.5	331	2	Q72B16	Q72b16 desulfovibr
844	63	12.5	540	2	Q66HP4	Q66hp4 rattus norv	917	62.5	12.5	348	2	Q8KBO8	Q8kbo8 chlorobium
845	63	12.5	576	2	Q641P2	Q641p2 mus musculu	918	62.5	12.5	361	1	COBT_MYCBO	P63842 mycobacteri
846	63	12.5	578	2	Q82RM4	Q82rm4 streptomyce	919	62.5	12.5	361	1	COBT_MYCTTU	P63841 mycobacteri
847	63	12.5	597	2	Q6C2X7	Q6c2x7 yarrowia 11	920	62.5	12.5	368	2	Q8G3D4	Q8g3d4 bruceella su
848	63	12.5	607	2	Q87XC4	Q87xc4 pseudomonas	921	62.5	12.5	372	2	Q6FNG9	Q6fng9 candida gla
849	63	12.5	614	2	Q65D36	Q65d36 bacillus 11	922	62.5	12.5	373	2	Q6N3Y9	Q6n3y9 rhodopseudo
850	63	12.5	620	2	Q6EUS5	Q6eus5 oryza sativ	923	62.5	12.5	375	2	Q6MNU9	Q6mnu9 methanococ
851	63	12.5	620	2	Q9PEF3	Q9pef3 xyloella fas	924	62.5	12.5	380	2	Q7UGD5	Q7ugd5 rhodopirell
852	63	12.5	634	2	Q9W646	Q9w646 oryzaia lat	925	62.5	12.5	388	2	Q8UC90	Q8uc90 agrobacteri
853	63	12.5	662	2	Q64UP4	Q64up4 bacteroides	926	62.5	12.5	393	2	Q84BB5	Q84bb5 erwina chr
854	63	12.5	662	2	Q8A8T1	Q8a8t1 bacteroides	927	62.5	12.5	399	2	Q6Z4M0	Q6z4m0 oryza sativ
855	63	12.5	684	2	Q9S282	Q9s282 streptomyce	928	62.5	12.5	401	2	Q9HXQ8	Q9hxq8 pseudomonas
856	63	12.5	694	2	Q7W1S8	Q7w1s8 bordetella	929	62.5	12.5	403	2	Q64ZQ8	Q64zq8 bacteroides
857	63	12.5	700	2	Q95TW3	Q95tw3 drosophila	930	62.5	12.5	404	2	Q7WOW5	Q7wow5 bordetella
858	63	12.5	739	2	Q89VS0	Q89vs0 bradyrhizob	931	62.5	12.5	408	2	Q80VU9	Q80v19 mus musculu
859	63	12.5	740	2	Q9N3Z2	Q9n3z2 caenorhabdi	932	62.5	12.5	408	2	Q80VU9	Q80v19 mus musculu
860	63	12.5	744	2	Q6N0U4	Q6n0u4 rhodopseudo	933	62.5	12.5	417	2	Q7NKKV3	Q7nkv3 gloebacteri
861	63	12.5	825	2	Q8P5T1	Q8p5t1 xanthomonas	934	62.5	12.5	419	2	Q8RGS7	Q8rgs7 fusobacteri
862	63	12.5	849	2	Q98E97	Q98e97 rhizobium 1	935	62.5	12.5	426	2	Q4Z5Y3	Q4z5y3 arabidopsis
863	63	12.5	874	1	CLPB_BRUME	Q8y91 bruceella me	936	62.5	12.5	426	2	Q9CAQ6	Q9caq6 arabidopsis
864	63	12.5	874	1	CLPB_BRUSU	Q7ce66 bruceella su	937	62.5	12.5	427	2	Q87VY5	Q87vy5 pseudomonas
865	63	12.5	880	2	Q63VRS	Q63vrs burkholderi	938	62.5	12.5	430	2	Q8VR17	Q8vr17 serratia ma
866	63	12.5	891	2	Q7T2X3	Q7t2x3 gallus gall	939	62.5	12.5	430	2	Q72K00	Q72k00 thermus the
867	63	12.5	932	1	PKM1_HUMAN	P54277 homo sapien	940	62.5	12.5	443	2	Q6ACB3	Q6acb3 leifsonia x
868	63	12.5	947	2	Q8RUT5	Q8ruts oryza sativ	941	62.5	12.5	445	2	Q9P1E2	Q9p1e2 campylobact
869	63	12.5	955	2	Q9W484	Q9w484 drosophila	942	62.5	12.5	450	2	Q7NCV5	Q7ncv5 gloebacter
870	63	12.5	988	2	Q6AMU1	Q6aw1 drosophila	943	62.5	12.5	458	2	Q881S7	Q881s7 pseudomonas
871	63	12.5	988	2	Q9W0Z3	Q9w0z3 drosophila	944	62.5	12.5	462	2	Q82CD6	Q82cd6 streptomyce
872	63	12.5	1062	1	NAL2_HUMAN	Q9nx02 homo sapien	945	62.5	12.5	463	2	Q6MVCU7	Q6mcv7 paracanthamyd
873	63	12.5	1145	2	Q7OHF8	Q7qth8 anopheles g	946	62.5	12.5	485	2	Q6N592	Q6n592 rhodopseudo
874	63	12.5	1153	2	Q7PSX6	Q7psx6 anopheles g	947	62.5	12.5	485	2	Q87V77	Q87v77 pseudomonas
875	63	12.5	1157	2	Q27088	Q27088 trichomonas	948	62.5	12.5	511	1	NAD8_CAU	Q9a43 caulobacter
876	63	12.5	1174	2	Q89N18	Q89n18 bradyrhizob	949	62.5	12.5	511	2	Q983V2	Q983v2 rhizobium 1
877	63	12.5	1299	2	Q8TXZ8	Q8txz8 methanopyru	950	62.5	12.5	513	2	Q9SRY1	Q9sry1 arabidopsis
878	63	12.5	1472	2	Q91214	Q91214 streptomyce	951	62.5	12.5	517	2	Q6DSW7	Q6dsw7 erwina car
879	63	12.5	1500	2	Q7QCC9	Q7qcg9 giardia lam	952	62.5	12.5	523	2	Q9C5L3	Q9c5l3 arabidopsis
880	63	12.5	1677	2	Q00805	Q00805 leishmania	953	62.5	12.5	557	2	Q741P4	Q741p4 mycobacteri
881	63	12.5	2137	2	Q84BQ6	Q84bq6 pseudomonas	954	62.5	12.5	560	1	BFS_MOUSE	Q64355 mus musculu
882	63	12.5	5541	2	Q6W5P9	Q6w5p9 streptomyce	955	62.5	12.5	560	2	Q8BSX4	Q8bsx4 mus musculu
883	63	12.5	74	2	Q9FBL3	Q9fbl3 streptomyce	956	62.5	12.5	560	2	Q8KOF6	Q8kof6 mus musculu
884	62.5	12.5	75	2	Q6A4X1	Q6a4x1 malus domes	957	62.5	12.5	573	2	Q8RVZ7	Q8rvz7 delinococcus
885	62.5	12.5	102	2	Q6C190	Q6c190 yarrowia 11	958	62.5	12.5	599	2	Q8TXZ7	Q8txz7 homo sapien
886	62.5	12.5	112	2	Q8LC40	Q8lc40 arabidopsis	959	62.5	12.5	601	2	Q300J9	Q300j9 archaeoglob
887	62.5	12.5	113	2	Q6N6R7	Q6n6r7 rhodopseudo	960	62.5	12.5	612	2	Q7NYO6	Q7nyo6 chromobacte
888	62.5	12.5	115	2	Q8USH4	Q8ush4 agrobacteri	961	62.5	12.5	618	2	Q914B7	Q914b7 pseudomonas
889	62.5	12.5	149	2	Q889R1	Q889r1 pseudomonas	962	62.5	12.5	633	2	Q8MLA8	Q8mla8 drosophila
890	62.5	12.5	150	2	Q88P31	Q88p31 xanthomonas	963	62.5	12.5	634	2	Q6A8V3	Q6a8v3 propionibac
891	62.5	12.5	151	2	Q6W8W9	Q6w8w9 pseudomonas	964	62.5	12.5	652	2	Q8G1R3	Q8g1r3 bruceella su
892	62.5	12.5	157	2	Q72G77	Q72g77 thermus the	965	62.5	12.5	662	2	Q6CON9	Q6con9 yarrowia 11
893	62.5	12.5	192	2	Q8VKM1	Q8vkm1 mycobacteri	966	62.5	12.5	680	2	Q95TU3	Q95tu3 drosophila
894	62.5	12.5	195	2	Q93NU6	Q93nu6 uncultured	967	62.5	12.5	685	2	Q8YGS9	Q8ygs9 bruceella me
895	62.5	12.5	209	2	Q93NTE	Q93nte uncultured	968	62.5	12.5	710	2	Q67P71	Q67p71 symbiobacte
896	62.5	12.5	216	2	Q72GUT	Q72gut7 thermus the	969	62.5	12.5	738	1	CPO_DROME	Q01617 drosophila
897	62.5	12.5	244	2	Q93NV4	Q93nv4 desulfovibr	970	62.5	12.5	760	1	CO2_MOUSE	Q2180 mus musculu
898	62.5	12.5	246	2	Q7W111	Q7w111 bordetella	971	62.5	12.5	760	1	Q70J50	Q70j50 mus musculu
899	62.5	12.5	251	2	Q7VZ36	Q7vz36 bordetella	972	62.5	12.5	802	2	Q81UM7	Q81um7 homo sapien
900	62.5	12.5	251	2	Q7W8P5	Q7w8p5 bordetella	973	62.5	12.5	802	2	Q8N8S5	Q8n8s5 homo sapien
901	62.5	12.5	251	2	Q7WK45	Q7wk45 bordetella	974	62.5	12.5	802	2	Q8BGD7	Q8bgd7 mus musculu
902	62.5	12.5	266	2	Q8G8G0	Q8g8g0 wolinetella s	975	62.5	12.5	802	2	Q8CJH6	Q8cjh6 rattus norv
903	62.5	12.5	267	1	THIG_DEIRA	Q8ryy1 deinococcus	976	62.5	12.5	904	2	Q75017	Q75017 ashbya gos
904	62.5	12.5	271	2	Q8T1T0	Q8t1t0 methanobarc	977	62.5	12.5	909	2	Q5Z585	Q5z585 pseudomonas
905	62.5	12.5	283	2	Q83J06	Q83j06 enterococcu	978	62.5	12.5	917	2	Q9ZMQ1	Q9zmq1 pseudomonas
906	62.5	12.5	284	2	Q34174	Q34174 pseudomonas	979	62.5	12.5	956	2	Q8VIG0	Q8vig0 mus musculu
907	62.5	12.5	284	2	Q7W0X7	Q7w0x7 bordetella	980	62.5	12.5	967	2	Q9BJZ5	Q9bjz5 drosophila

981	62.5	12.5	970	2	Q9VN28	Q9vn28 drosophila	1054	62	12.4	408	2	Q7YX47	Q7yx47 bordetella
982	62.5	12.5	1949	2	Q6VMW9	Q6vmw9 human cytom	1055	62	12.4	408	2	Q7WLE6	Q7wle6 bordetella
983	62.5	12.5	1224	2	Q9VXW2	Q9vxw2 drosophila	1056	62	12.4	409	2	Q8PLJ9	Q8plj9 xanthomonas
984	62.5	12.5	1087	2	Q8BTE7	Q8bte7 homo sapien	1057	62	12.4	426	2	Q92U73	Q92u73 rhizobium
985	62.5	12.5	2008	2	Q9G5S8	Q9g5s8 homo sapien	1058	62	12.4	431	2	Q8XYF5	Q8xyf5 ralscoulia
986	62.5	12.5	2146	2	Q8IZY2	Q8izy2 homo sapien	1059	62	12.4	433	2	Q6NTN0	Q6ntn0 rhodospira
987	62.5	12.5	2146	2	Q9NR73	Q9nr73 homo sapien	1060	62	12.4	443	2	Q67N88	Q67n88 symbiobac
988	62.5	12.5	2680	2	Q7PP92	Q7pp92 atophales g	1061	62	12.4	446	1	MURF_STRO	Q3804 streptomy
989	62.5	12.5	2873	2	Q93075	Q93075 gb virus c/	1062	62	12.4	464	2	Q8U2D9	Q8u2d9 ceratoph
990	62.5	12.5	3295	2	Q83X71	Q83x71 streptomyce	1063	62	12.4	474	2	Q6G6H1	Q6g6h1 yersinia
991	62	12.4	98	2	Q9KEE3	Q9kee3 bacillus ha	1064	62	12.4	474	2	Q8ZJ57	Q8zj57 yersinia
992	62	12.4	117	2	Q24440	Q24440 phaeosolus v	1065	62	12.4	486	2	Q6MKU6	Q6mku6 bdellovib
993	62	12.4	128	1	RL7_CORGL	RL7 CORGL	1066	62	12.4	486	2	Q6KUN6	Q6kun6 xanthomon
994	62	12.4	137	2	Q8FSA0	Q8fse0 corynebacte	1067	62	12.4	494	2	Q52206	Q52206 rhodospir
995	62	12.4	137	2	Q9YFS5	Q9yfs5 aeropyrum p	1068	62	12.4	500	2	Q9AHU8	Q9ah8 xanthomon
996	62	12.4	142	2	Q6HLD5	Q6hld5 human adeno	1069	62	12.4	502	2	Q74JH0	Q74jh0 halobacte
997	62	12.4	144	2	Q8POV1	Q8pov1 xanthomonas	1070	62	12.4	535	2	Q6E7A7	Q6e7a7 yersinia
998	62	12.4	150	2	Q87BM9	Q87bm9 xylolla fae	1071	62	12.4	535	2	Q8ZHP8	Q8zhp8 rhizobium
999	62	12.4	156	2	Q67KD9	Q67kd9 symbiobacte	1072	62	12.4	541	2	Q92243	Q92243 rhizobium
1000	62	12.4	164	2	Q72LCL	Q72lcl thermus the	1073	62	12.4	544	2	Q8H4X9	Q8h4x9 yersinia
1001	62	12.4	188	2	Q6Z2Y5	Q6z2y5 oryza sativ	1074	62	12.4	545	2	Q84KX9	Q84kx9 beta vulg
1002	62	12.4	199	1	IL11_RAT	IL11 rat	1075	62	12.4	549	2	P93076	P93076 oryza sat
1003	62	12.4	200	2	Q6S585	Q6s585 ratius noty	1076	62	12.4	550	2	P93075	P93075 beta vulg
1004	62	12.4	211	2	Q937M4	Q937m4 arabidopsis	1077	62	12.4	574	2	Q9AQH1	Q9aqh1 pseudomon
1005	62	12.4	219	2	Q6NM02	Q6nm02 arabidopsis	1078	62	12.4	574	2	Q9AHG7	Q9ahg7 pseudomon
1006	62	12.4	224	2	Q6ZD78	Q6zd78 oryza sativ	1079	62	12.4	584	2	Q8XZC6	Q8xc6 ralscoulia
1007	62	12.4	232	2	Q6N0Q1	Q6n0q1 rhodopseudo	1080	62	12.4	585	2	Q6NS33	Q6ns33 rhodopseu
1008	62	12.4	235	2	Q96VD8	Q96vd8 ussilaago ma	1081	62	12.4	591	2	Q8CP81	Q8c81 mus muscu
1009	62	12.4	240	2	Q654S3	Q654s3 oryza sativ	1082	62	12.4	594	2	Q9XKH3	Q9xkh3 mus muscu
1010	62	12.4	242	2	Q8EGZ0	Q8egz0 shewanella	1083	62	12.4	609	2	Q6E158	Q6e158 bacillus h
1011	62	12.4	252	1	HIS4_HALT1	Q9hm14 halobacteri	1084	62	12.4	620	1	SMP_COTJA	Q671FL1 symbiob
1012	62	12.4	257	2	MOAE_KLEAE								

1273	61.5	12.3	3247	2	065553	065553 bovine herp	1346	61	12.2	370	2	0887D7	0887d7 pseudomonas
1274	61.5	12.3	3247	2	077CD4	077cd4 bovine herp	1347	61	12.2	370	2	0887D7	0887d7 pseudomonas
1275	61.5	12.3	3889	2	06SSB8	06sse8 chlamydomon	1348	61	12.2	377	2	09KYT3	09kyt3 ralestonia s
1276	61.5	12.3	4753	2	08PLI3	08pli3 xanthomonas	1349	61	12.2	377	2	09KYT3	09kyt3 streptomyc
1277	61.5	12.3	4881	2	09S0R3	09s0r3 streptomyc	1350	61	12.2	382	2	09KS54	09ksb4 desulfobact
1278	61	12.2	104	2	08TFV6	08tfv6 aspergillus	1351	61	12.2	390	2	022101	022101 caenorhabdi
1279	61	12.2	104	2	08TFV7	08tfv7 aspergillus	1352	61	12.2	392	2	08CCU7	08ccu7 mus musculi
1280	61	12.2	106	2	08TFV3	08tfv3 aspergillus	1353	61	12.2	394	1	Y169_SYNFX	P59921 synchococ
1281	61	12.2	107	2	08TFV2	08tfv2 aspergillus	1354	61	12.2	395	2	09RVT4	09rvt4 delnoco
1282	61	12.2	115	2	059996	059996 neosartorya	1355	61	12.2	396	2	06RTT3	06rtt3 xenopus lae
1283	61	12.2	115	2	06A9H0	06a9h0 propionibac	1356	61	12.2	398	1	SUCC_RHIME	09ey99 rhizobium m
1284	61	12.2	117	2	09KN10	09kn10 vibrio chol	1357	61	12.2	402	2	06H144	06h144 bacillus th
1285	61	12.2	126	2	09HHE1	09heh1 halobacteri	1358	61	12.2	406	2	06SF87	06sf87 bacillus th
1286	61	12.2	142	2	08UY87	08uy87 simian aden	1359	61	12.2	406	2	06MA90	06ma90 paracellamyd
1287	61	12.2	142	2	06OPB5	06opb5 simian aden	1360	61	12.2	409	2	09KX33	09kx33 bacillus ha
1288	61	12.2	143	2	067R71	067r71 symbiobacte	1361	61	12.2	414	2	08G0Z7	08g0z7 bruceella su
1289	61	12.2	144	2	062AY7	062ay7 burkholderi	1362	61	12.2	419	2	097RL7	09gr71 streptococ
1290	61	12.2	145	2	06DB51	06db51 erwina car	1363	61	12.2	419	2	08DOF7	08dqf7 streptococ
1291	61	12.2	150	2	06N8J3	06n8j3 rhodospseudo	1364	61	12.2	419	2	09RIT4	09rit4 streptomyc
1292	61	12.2	152	2	09RNR7	09rnr7 solar lake	1365	61	12.2	419	2	06MAE1	06mae1 paracellamyd
1293	61	12.2	167	2	08PH36	08ph36 xanthomonas	1366	61	12.2	420	1	UE38_DEIRA	09rue8 deinococcus
1294	61	12.2	172	2	0916Y7	0916y7 pseudomonas	1367	61	12.2	420	2	09CTE5	09cte5 pasteurella
1295	61	12.2	185	1	ADH_ANAPL	0916y7 pseudomonas	1368	61	12.2	422	2	092TW0	092tw0 rhizobium m
1296	61	12.2	190	2	08HHK6	08hhk6 anas platyr	1369	61	12.2	424	2	073T89	073t89 mycobacteri
1297	61	12.2	190	2	08HHK6	08hhk6 sphenodon p	1370	61	12.2	424	2	0743Z9	0743z9 mycobacteri
1298	61	12.2	191	2	07XZ45	07xz45 sphenodon p	1371	61	12.2	430	2	08G3M5	08g3m5 bifidobacte
1299	61	12.2	192	2	08R1T7	08r1t7 griffithia	1372	61	12.2	433	1	CITM_BACSU	P55069 bacillus su
1300	61	12.2	194	2	09ATC7	09atc7 mus musculi	1373	61	12.2	434	2	06NEU9	06neu9 corynebacte
1301	61	12.2	199	1	ITL1_MOUSE	09atc7 vaucheria l	1374	61	12.2	435	2	07UXZ6	07uxz6 corynebacte
1302	61	12.2	203	2	070A08	P47873 mus musculi	1375	61	12.2	440	2	06LP21	06lp21 rhodospirell
1303	61	12.2	207	2	027558	070ag8 nonomurea	1376	61	12.2	443	2	08RKZ4	08rkz4 photobacter
1304	61	12.2	215	2	06C7P7	027558 methanobact	1377	61	12.2	447	2	082510	082510 streptomyc
1305	61	12.2	228	2	08U269	06c7p7 yarrowia ll	1378	61	12.2	449	2	045082	045082 streptomyc
1306	61	12.2	228	2	089HH9	08u269 pyrococcus	1379	61	12.2	449	2	089IL4	089il4 burkholderi
1307	61	12.2	231	2	06N634	089h9 bradyrhizob	1380	61	12.2	463	2	06NGY8	089il4 bradyrhizob
1308	61	12.2	232	2	07N4F6	06n634 rhodospseudo	1381	61	12.2	480	2	09RVA7	06asg6 corynebacte
1309	61	12.2	234	2	093HB2	07n4f6 photorhabdu	1382	61	12.2	487	2	09VC70	06asg6 propionibac
1310	61	12.2	240	2	07VZ11	093hb2 streptomyc	1383	61	12.2	493	2	09VUZ4	09vr87 deinococcus
1311	61	12.2	240	2	07W559	07vz11 bordetella	1384	61	12.2	499	2	08B3C6	09vuz4 aeropyrum p
1312	61	12.2	240	2	07WDB6	07w559 bordetella	1385	61	12.2	500	2	06N7D8	09vuz4 drosophila
1313	61	12.2	246	2	082VC7	07wdb6 bordetella	1386	61	12.2	504	2	08G5A1	08g5a1 rhodospseudo
1314	61	12.2	249	2	08YSS1	082vc7 nitrosomona	1387	61	12.2	504	2	06LNS1	08g5a1 bifidobacte
1315	61	12.2	259	2	026573	08y8s1 anabaena sp	1388	61	12.2	512	2	07PVP6	06lms1 photobacter
1316	61	12.2	261	2	06CMD7	026573 methanobact	1389	61	12.2	520	2	08PFW2	07pvp6 anophelies g
1317	61	12.2	265	2	069LD4	06cmd7 kluyveromyc	1390	61	12.2	523	2	080ZE2	08pfw2 xanthomonas
1318	61	12.2	267	2	09X919	069ld4 oryza sativ	1391	61	12.2	525	2	005685	080ze2 mus musculi
1319	61	12.2	277	2	07VT83	09x919 streptomyc	1392	61	12.2	540	1	08EMW1	005685 mycobacteri
1320	61	12.2	280	2	07X4W4	07vt83 bordetella	1393	61	12.2	562	1	ATKA_ALIAC	08emw1 oceanobacti
1321	61	12.2	281	2	041345	07x4w4 rhodospirill	1394	61	12.2	562	1	073TO3	09xe11 alicyclobac
1322	61	12.2	281	2	042407	041345 silene prat	1395	61	12.2	572	2	P87247	09xe11 mycobacteri
1323	61	12.2	295	1	ADP9_MOUSE	042407 mus musculi	1396	61	12.2	575	2	07P9Z3	P87247 botrytis cl
1324	61	12.2	305	2	06C9U8	09jjj3 mus musculi	1397	61	12.2	578	2	07NMT5	07nmt5 rickettsia
1325	61	12.2	305	2	09P8M1	06c9u8 yarrowia ll	1398	61	12.2	579	2	08CS41	07nmt5 gloobacter
1326	61	12.2	312	2	09EMZ9	09p8m1 yarrowia ll	1399	61	12.2	582	2	09HT97	08cs41 mus musculi
1327	61	12.2	313	2	09X5I8	09emz9 streptomyc	1400	61	12.2	586	1	S132_MOUSE	09ht97 pseudomonas
1328	61	12.2	313	2	09X5I8	09x5i8 anophelies g	1401	61	12.2	589	1	09RUH5	09rue8 mus musculi
1329	61	12.2	313	2	07W2A6	09x5i8 neisseria m	1402	61	12.2	615	2	096AS7	09rue8 mus musculi
1330	61	12.2	313	2	07WR73	07w2a6 bordetella	1403	61	12.2	615	2	096CK0	09rue8 delnoco
1331	61	12.2	313	2	08BL10	08bl10 pseudomonas	1404	61	12.2	615	2	096CK0	09rue8 delnoco
1332	61	12.2	314	2	07XR51	07xr51 oryza sativ	1405	61	12.2	620	2	07W7A0	096ck0 homo sapien
1333	61	12.2	314	2	08PCJ3	08pcj3 xanthomonas	1406	61	12.2	630	1	ACHA_RAT	096ck0 xylella fas
1334	61	12.2	330	1	TH14_FUSOX	P23618 fustarium ox	1407	61	12.2	637	1	PUE8_DROME	P09483 rattus norv
1335	61	12.2	339	2	08BRD8	09k004 neisseria m	1408	61	12.2	641	2	08BVT0	08bvt0 mus musculi
1336	61	12.2	339	2	08BRD8	08brd8 pseudomonas	1409	61	12.2	671	2	09N9L9	09n9l9 leishmania
1337	61	12.2	330	2	08PZ52	08pzd5 mechanosarc	1410	61	12.2	682	2	08C0P2	08c0p2 mus musculi
1338	61	12.2	333	2	08FXZ5	08fxz5 bruceella su	1411	61	12.2	685	2	06SX51	06sx51 oryza sativ
1339	61	12.2	345	2	06N0W8	06n0w8 corynebacte	1412	61	12.2	694	2	07W714	07w714 bordetella
1340	61	12.2	347	2	P94802	P94802 halocitax s	1413	61	12.2	712	2	07KUP1	07kup1 drosophila
1341	61	12.2	349	2	09FEBZ8	09febz8 streptomyc	1414	61	12.2	723	2	08Y2S0	08y2s0 mycobacteri
1342	61	12.2	355	1	LPXD_AGRTS	08uf15 agrobacteri	1415	61	12.2	732	2	09KHM5	09khm5 syncytiococ
1343	61	12.2	359	1	Y199_MYCTU	08uf15 agrobacteri	1416	61	12.2	732	2	08T6L2	08t6l2 giardia lam
1344	61	12.2	364	2	093RV8	093rv8 streptomyc	1417	61	12.2	738	2	060BQ3	060bq3 chlamydomon
1345	61	12.2	365	2	09A2P7	09a2p7 caulobacter	1418	61	12.2	738	2	060BQ3	060bq3 chlamydomon

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stanclevon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE OF 21-35.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION. Potential growth inhibitory cytokine.
 CC -1- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in
 CC breast cancer cell lines.
 CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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DR EMBL; AY040564; AAK82942.1; -
 DR EMBL; AF313458; AAL26217.1; -
 DR EMBL; AF316839; AAO04481.1; -
 DR EMBL; AY350864; AAO89423.1; -
 DR EMBL; BC029176; AAH29176.1; -
 DR GeneW; HGNC:18384; SCGB3A1.
 DR H-InvDB; HIX0005498; -
 DR MIM; 606500; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005125; P:cytokine activity; NAS.
 DR GO; GO:0030308; P:negative regulation of cell growth; NAS.
 DR GO; GO:0042127; P:regulation of cell proliferation; NAS.
 KM Cytokine; Direct protein sequencing; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 104 Uteroglobin-related protein 2.
 FT COMPLET 19 19 A--R (in Ref. 1).
 SQ SEQUENCE 104 AA; 10100 MW; C1A0951F8F81455F CRC64;

Query Match 100.0%; Score 502; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-36;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLAALGLCVALLSCSSAAAFVSGAKPVAQPAALLESAAEAGAGTLANPLGTNPL 60
 Db 1 MKLAALGLCVALLSCSSAAAFVSGAKPVAQPAALLESAAEAGAGTLANPLGTNPL 60
 QY 61 LSSLGLIPVNHLEGSQKCVAEIGPQAVGAVKALIKALLGLTAVFG 104
 Db 61 LSSLGLIPVNHLEGSQKCVAEIGPQAVGAVKALIKALLGLTAVFG 104

RESULT 2

Q71MT8
 ID Q71MT8 PRELIMINARY; PRT; 104 AA.
 AC Q71MT8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Pseudo secretory protein 2.
 GN Name=Pns2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar;
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knoops B.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF436841; AA004483.1; -
 SQ SEQUENCE 104 AA; 10512 MW; FDB870D75750F9E6 CRC64;

Query Match 52.0%; Score 261; DB 2; Length 104;
 Best Local Similarity 59.8%; Pred. No. 2, 7e-15;
 Matches 64; Conservative 13; Mismatches 24; Indels 6; Gaps 4;
 QY 1 MKLAAL-LGLCVALLSCSSAAAFVSGAKPVAQPAALLESAAEAGAGTLAN-PLGTNPL 57
 Db 1 MKLTAFVFCVALLSDGVAFFVDSLAKPVPEVPAALAAEAVNGAVSPLSHLAIL 60
 QY 58 KLLSLGLIPVNHLEGSQKCVAEIGPQAVGAVKALIKALLGLTAVFG 104
 Db 61 RLTLASLGLIPVNHLEGSQKCVAEIGPQAVGAVKALIKALLGLTAVFG 104

RESULT 3
 UGR2_MOUSE
 ID UGR2_MOUSE STANDARD; PRT; 104 AA.
 AC Q920D7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
 DE normal-1) (Secretoglobin family 3A member 1) (Pneumo secretory protein
 DE 2) (Pns2-2).
 GN Name=Scgb3a1; Synonyms=Hn1l, Pns2, UGRP2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21396515; PubMed=11481438; DOI=10.1073/pnas.171138398;
 RA Krop I.E., Syroel D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
 RA Kaelin C.M., Rhee E., Rosenberg M., Schmitt S., Marks J.R., Pagon Z.,
 RA Belina D., Razumovic J., Poljak K.;
 RT "HIN-1, a putative cytokine highly expressed in normal but not
 RT cancerous mammary epithelial cells";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2159178; PubMed=11682631; DOI=10.1210/me.15.11.2021;
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
 RA Kimura S.;
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
 RT a novel lung-enriched downstream target gene for the T/BBP/NKX2.1
 RT homeodomain transcription factor";
 RL Mol. Endocrinol. 15:2021-2036(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knoops B.;
 RT "Molecular cloning of Pns2-1, a protein of the respiratory tract with
 RT potential association to atopy";
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Potential growth inhibitory cytokine.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
 CC -----
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 CC -----
 DR EMBL: AF313456; AAL26216.1; -.
 DR EMBL: AF436840; AAQ04482.1; -.
 DR MGD; MGI:1915912; Scg3a1.
 KW Cytokine; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 104 Uteroglobin-related protein 2.
 SQ SEQUENCE 104 AA; 10591 MW; D62F0B601FB57A6D CRC64;
 Query Match 49.8%; Score 250; DB 1; Length 104;
 Best Local Similarity 57.0%; Pred. No. 2.5e-14;
 Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;
 QY 1 MKLAAALIGCVALLSCSSAAAFVGS-AKPVAQPVAALESAAEAGATLAN-PLGTINPL 57
 DB 1 MKLTTPLVLCVALLSDSGVAFPMDSIAKPAVEPVAAALAAVAGAVPSLPLSHLAIL 60
 QY 58 KLLLSLGIPIVNHLESGOKVCAELGPOAVGAVKALKALGALTIVG 104
 DB 61 RFLIAMSIGIPLDPLIESRKCVTELGPBAVGAV--KSLIGVLTIVG 104
 RESULT 4
 Q7M741 PRELIMINARY; PRT; 93 AA.
 ID 07M741;
 AC 07M741;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE HINI (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=22338213; PubMed=12406855;
 RA Reynolds S.D., Reynolds P.R., Pryhuber G.S., Finder J.D., Stripp B.R.;
 RT "Secretoglobins SCGB3A1 and SCGB3A2 define secretory cell subsets in
 RT mouse and human airways.";
 RL Am. J. Respir. Crit. Care Med. 166:1498-1509(2002).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL: BK000202; DAA00359.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 93 AA; 9319 MW; D3E2F96A9380DF70 CRC64;
 Query Match 46.2%; Score 232; DB 2; Length 93;
 Best Local Similarity 57.1%; Pred. No. 8.5e-13;
 Matches 56; Conservative 15; Mismatches 19; Indels 8; Gaps 4;
 QY 9 LCVALSCSSAAAFVGS-AKPVAQPVAALESAAEAGATLAN-PLGTINPLKLLSLSLGI 66
 DB 2 LCVL---VGAFLVSLAKPAVEPVAAALAAVAGAVPSLPLSHLAILRIVSLGI 58
 QY 67 PVNHLESGOKVCAELGPOAVGAVKALKALGALTIVG 104
 DB 59 PLDPLIDGSRKCVTELGPBAVGAV--KSLIGALTIVG 93
 RESULT 5
 Q8CJC6

ID Q8CJC6 PRELIMINARY; PRT; 94 AA.
 AC Q8CJC6;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE UGRP2 type B.
 GN Name=Scg3a1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=22326074; PubMed=12438750; DOI=10.1159/000064067;
 RA Nimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Sztosdal A.,
 RA Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.;
 RT "Cloning, expression, and chromosomal localization of the mouse gene
 RT (Scg3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-
 RT related protein gene family.";
 RL Cytogenet. Genome Res. 97:120-127(2002).
 DR EMBL: AF313457; AAN62328.1; -.
 DR MGD; MGI:1915912; Scg3a1.
 DR GO; GO:0005615; Extracellular space; TAS.
 SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;
 Query Match 44.8%; Score 225; DB 2; Length 94;
 Best Local Similarity 57.3%; Pred. No. 3.5e-12;
 Matches 51; Conservative 14; Mismatches 20; Indels 4; Gaps 2;
 QY 17 SAAAFVGSAPVAPVAALESAAEAGATLAN-PLGTINPLKLLSLGIPIVNHLEGS 75
 DB 9 SVAFFWDSLAKPAVEPVAAALAAVAGAVPSLPLSHLAILRFLIAMSIGIPLDPLIES 68
 QY 76 QKCVAEIPQAVGAVKALKALGALTIVG 104
 DB 69 RKCVELGPBAVGAV--KSLIGVLTIVG 94
 RESULT 6
 UGR1_HUMAN
 ID UGR1_HUMAN STANDARD; PRT; 93 AA.
 AC Q96PL1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
 DE member 2) (Pneumo secretory protein 1) (Pnsp-1) (UNQ566/PRO1128).
 GN Name=SCGB3A2; Synonyms=PNSP1, UGRP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=21539178; PubMed=11682631; DOI=10.1210/me.15.11.2021;
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
 RA Kimura S.;
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
 RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
 RT homeodomain transcription factor.";
 RL Mol. Endocrinol. 15:2021-2036(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Clippe A., Lating I.A., Lesouef P.N., Bernard A., Knoops B.;
 RT "Molecular cloning of Pnsp-1, a protein of the respiratory tract with
 RT potential association to atopy.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,

RA Huang A., Kim H.S., Klimoweki L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh U., Smith V., Stinson J., Vagstad A.,
 RA Vanden R., Watson C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godoweki P., Gray A.;
 RT "The secreted protein discovery initiative (SDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadleron M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scheraga J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SUBUNIT: Homodimer.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
 CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
 CC -----
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DR EMBL; AF313455; AAL26215.1; -
 DR EMBL; AF439544; AA004559.1; -
 DR EMBL; AF439545; AA004560.1; -
 DR EMBL; AY388979; AA089358.1; -
 DR EMBL; BC024232; AAH24232.1; -
 DR Gene; HGNC:18391; SCGB3A2.
 DR H-InvDB; HIX0005286; -
 DR MIM; 606531; -
 KW Signal.
 FT CHAIN 1 21 Potential.
 FT SIGNAL 93 Uteroglobin-related protein 1.
 SQ SEQUENCE 93 AA; 10161 MW; FBD4BFC2BF3718 CRC64;

Query Match 31.9%; Score 160; DB 1; Length 93;
 Best Local Similarity 43.6%; Pred. No. 1.7e-06;
 Matches 44; Conservative 9; Mismatches 38; Indels 10; Gaps 2;

QY 1 MKLAALGLCVSLSCG-SAAFLVGSAAKPVAPVVALESAAAGAGTLANPLGTINPLKT 59
 Db 1 MKLVITFLVTLTSLCYSATAPFLINKVPLPVDKLPL-----PLDNLIPFMDPLK 51
 QY 60 LLSLGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100
 Db 52 LKLTIGISVEHLVEGRKCVNELGEPSEAVKLLALSHL 92

RESULT 7
 ID 071MM7 PRELIMINARY; PRT; 93 AA.
 AC 071MM7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Pseudo secretory protein 1.
 GN Name=Pnsp1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar;
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knops B.;
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439547; AA004562.1; -
 SQ SEQUENCE 93 AA; 10042 MW; EC633755701E3076 CRC64;

Query Match 29.6%; Score 148.5; DB 2; Length 93;
 Best Local Similarity 40.8%; Pred. No. 1.7e-05;
 Matches 40; Conservative 10; Mismatches 35; Indels 13; Gaps 2;

QY 3 LLAALGLCVSLSCGSSAAAFVGSAAKPVAPVVALESAAAGAGTLANPLGTINPLKT 62
 Db 8 LVTITIGIC---GYSATAPFLINSVPLPVDKLPL-----PLDNLIPFMDPLK 54
 QY 63 SGIGIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100
 Db 55 TLGIGISVEHLVEGRKCVNELGEPSEAVKLLALSHL 92

RESULT 8
 ID UGR1 MOUSE STANDARD; PRT; 139 AA.
 AC Q920H1; Q920H2; Q920H3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
 DE member 2) (Pseudo secretory protein 1) (Pnsp-1).
 GN Name=Scg3a2; Synonyms=Pnsp1, UGRP1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCI_TaxID=10090;
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RC TISSUE=Lung;
 RX MEDLINE=21539178; PubMed=11682631; DOI=10.1210/me.15.11.2021;
 RA Nimri T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
 RA Kimura S.;
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
 RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
 RT homeodomain transcription factor.";
 RL Mol. Endocrinol. 15:2021-2036(2001).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM A).
 RC STRAIN=NMRI;
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knops B.;
 RT "Molecular cloning of Pnsp-1, a protein of the respiratory tract with
 RT potential association to atopy.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=C;
 CC Name=A;
 CC IsoId=Q920H1-1; Sequence=Displayed;
 CC IsoId=Q920H1-2; Sequence=VSP_006727, VSP_006728;

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CC      Name=B;
CC      IsoId=Q920H1.3; Sequence=VSP_006726;
CC      TISSUE SPECIFICITY: Highly expressed in lung.
CC      -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC      -----
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CC      entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC      or send an email to license@1sb-sib.ch).
CC      -----
DR      EMBL: AF274959; AAL25708.1; -.
DR      EMBL: AF274960; AAL25709.1; -.
DR      EMBL: AF274961; AAL25710.1; -.
DR      EMBL: AF439546; AAO04561.1; -.
DR      MGI: 2153470; Scg3a2.
DR      GO: 0005576; C:extracellular; IDA.
DR      GO: 0005515; F:protein binding; IPI.
DR      InterPro: IPR006038; Uteroglobin_supf.
DR      Pfam: PF01099; Uteroglobin; 1.
KW      Alternative splicing; Signal.
FT      SIGNAL 1 21 Potential.
FT      CHAIN 22 139 Uteroglobin-related protein 1.
FT      VARSPLIC 107 139 VSVLFLPMICAYPRDSKKQTFARLERVEGSKL -> EALS
FT      VARSPLIC 107 139 HIV (in isoform B).
FT      VARSPLIC 85 91 /FTId=VSP_006726.
FT      VARSPLIC 92 139 /FTId=VSP_006727.
FT      VARSPLIC 92 139 /FTId=VSP_006728.
FT      VARSPLIC 92 139 /FTId=VSP_006728.
SQ      SEQUENCE 139 AA; 15431 MW; 8A2PB08B41B6554 CRC64;

Query Match 26.9%; Score 135; DB 1; Length 139;
Best Local Similarity 35.1%; Pred. No. 0.00037;
Matches 34; Conservative 17; Mismatches 36; Indels 10; Gaps 1;

QY      1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVAALSAEAAGTLANPLGLNPLKLL 60
DB      1 MKLVSIPLVLTIGICGYSATALLINRLPVVDKLPV-----PLDDIIPSFDPKML 50

QY      61 LSLGIIPVNHLEIGSQKVAELGPOAVGAKALKALL 97
DB      51 LKTLGISVEHVTGKKCVDELGPBSEAVKGLIVII 87

RESULT 9
Q82LN6 PRELIMINARY; PRT; 255 AA.
AC      082LN6;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Putative methionine aminopeptidase.
GN      OrderedLocustNames=SAV1974;
OS      Streptomyces avermitilis.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=33903;
RX      MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RX      Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA      Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA      Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT      "Genome sequence of an industrial microorganism Streptomyces
RT      avermitilis: deducing the ability of producing secondary
RT      metabolites."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RP      SEQUENCE FROM N.A.
RN      [2]
RP      SEQUENCE FROM N.A.

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RC      STRAIN=MA-4680;
RX      MEDLINE=22608306; PubMed=12692562;
RX      Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA      Sakaki Y., Hattori M., Omura S.;
RT      "Complete genome sequence and comparative analysis of the industrial
RT      microorganism Streptomyces avermitilis."
RL      Nat. Biotechnol. 21:526-531(2003).
CC      -1- FUNCTION: Removes the amino-terminal methionine from nascent
CC      proteins (By similarity).
CC      -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC      preferentially methionine, from peptides and arylamides.
CC      -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).
CC      -1- SIMILARITY: Belongs to peptidase family M24a.
DR      EMBL: AP005029; BAC69685.1; -.
DR      HSSP: Q9X117; 100X.
DR      GO: 0004239; F:methionyl aminopeptidase activity; IEA.
DR      GO: 0008233; F:peptidase activity; IEA.
DR      GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro: IPR002467; Pept_M24A_MAP.
DR      InterPro: IPR001714; Pept_M24A_MAP.
DR      Pfam: PF00557; Peptidase_M24_1.
DR      PRINTS: PR00599; MAPEPTIDASE.
DR      TIGRPFAMs: TIGR00500; met_pdae_1.
KW      Aminopeptidase; Cobalt; Complete proteome; Hydrolyase; Protease.
SQ      SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;

Query Match 17.5%; Score 88; DB 2; Length 255;
Best Local Similarity 31.6%; Pred. No. 8.2;
Matches 31; Conservative 16; Mismatches 19; Indels 32; Gaps 6;

QY      7 LGLCVA--LSCSSAAFLVGSAPVAPVAAL-----SAAEAGA--GTLANPL 51
DB      99 LBLAVARGVADAAISFLVGKAP-AESVAMTEATERALAGIAAKKGAIRIGDLSHAI 157

QY      52 GTLNPLKLLSLGIIPVNHLEIGSQKVAELGPOAVGA 89
DB      158 GT-----VLSKAGYPIIN-----TEFGSHGIGS 179

RESULT 10
Q8FST3 PRELIMINARY; PRT; 281 AA.
AC      08FST3;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
GN      OrderedLocustNames=CE0299;
OS      Corynebacterium efficiens.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX      NCBI_TaxID=152794;
RX      MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RX      Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA      Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA      Gojohori T.;
RT      "Comparative complete genome sequence analysis of the amino acid
RT      replacements responsible for the thermostability of Corynebacterium
RT      efficiens."
RL      Genome Res. 13:1572-1579(2003).
DR      EMBL: AP005215; BAC17109.1; -.
DR      InterPro: IPR01992; Bact_sec_systII.
DR      Pfam: PF00482; GSP11_F_1.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 281 AA; 28188 MW; 3143B69C35048C2D CRC64;

Query Match 16.6%; Score 83.5; DB 2; Length 281;
Best Local Similarity 30.1%; Pred. No. 22;
Matches 40; Conservative 9; Mismatches 45; Indels 39; Gaps 7;

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FT      MUTAGEN      1184      1184      /FTId=VSP_004539.
FT      MUTAGEN      1291      1291      H->A: Loss of activity; when associated
FT      SEQUENCE      1327 AA; 142010 MW; E14DE985C710B957 CRC64;
FT      SEQUENCE      1327 AA; 142010 MW; E14DE985C710B957 CRC64;

Query Match      16.5%; Score 83; DB 1; Length 1327;
Best Local Similarity 30.5%; Pred. No. 99;
Matches 29; Conservativity 13; Mismatches 43; Indels 10; Gaps 3;

QY      15 CSSAAAFVGSAXPVAPVVALESAA-----EAGAGTIANPLGTLPKLKLLSLGIPV 69
      90 CSTTSTICTVAAAPVV-PAVSTSSAGAVAPNPAAGSGNNPSSSSPTSSSSSPSSPGS 148
      70 HLIBGSG---KCVAEIGPOAVGAVKALKLLGAL 100
      149 SLAESPEAGVSSSTAPLPGAGPGTGVPAVSGAL 183

Db

RESULT 12
QY      ID Q9K3G4      PRELIMINARY;      PRT;      247 AA.
AC      Q9K3G4;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Hypothetical protein SC01277.
GN      ORFNames=SCG18.24;
OS      Streptomyces coelicolor.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2) / M145;
RX      MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA      Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA      Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleiser H.,
RA      Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA      Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA      Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA      Rabinowitsch R., Rajandream M.A., Rutherford K.M., Ruter S.,
RA      Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA      Warren T., Wietorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA      Hopwood D.A.;
RT      "Complete genome sequence of the model actinomycete Streptomyces
RT      coelicolor A3(2).";
RL      Nature 417:141-147(2002).
RW      EMBL: AL939108; CAB99157.1; -.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 247 AA; 22950 MW; EE32ABD6146881B CRC64;

Query Match      16.4%; Score 82.5; DB 2; Length 247;
Best Local Similarity 31.8%; Pred. No. 24;
Matches 34; Conservativity 10; Mismatches 40; Indels 23; Gaps 5;

QY      17 SAAAFVGSAXP-----VAQPVAALESAAEAG-----AGTIANPLGTLP-----NPLKL 59
      61 NALAAAGAVNPAATAGVNPPLAALGGTGAAGPLAGLAAGAGPLGNTAGAAQNPLAA 120
      60 LLSLSL--GIIVNHLIESOKVAELGPOAVGAVKALKLLGALTVP 104
      121 LTGAAGGNNPLAALGAGNPLAALG---GAANPLAAVGAAGALG 163

Db

RESULT 13
QY      ID Q98CR1      PRELIMINARY;      PRT;      694 AA.
AC      Q98CR1;
DT      01-OCT-2001 (TREMBlrel. 18, Created)
DT      01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)

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DE      M15043 protein.
GN      OrderedLocuNames=m15043;
OS      Rhizobium loti (Mesorhizobium loti).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Phyllobacteriaceae; Mesorhizobium.
OX      NCBI_TaxID=381;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SRRAIN=MAFP303099;
RX      MEDLINE=21082930; PubMed=11214968;
RA      Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA      Matanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
RA      Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
RA      Mochizuki Y., Nakayama S., Nakazaki N., Shimpso S., Sugimoto M.,
RA      Takenuchi C., Yamada M., Tabara S.;
RT      "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT      Mesorhizobium loti.";
RL      DNA Res. 7:331-338(2000).
DR      EMBL: AP003005; BAB51560.1; -.
DR      InterPro: IPR003781; COA_binding.
DR      InterPro: IPR001412; tRNA_synt_I.
DR      Pfam: PF02629; COA_binding; 1.
DR      PROSITE: PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
KW      Complete proteome.
SQ      SEQUENCE 694 AA; 73126 MW; 19E4978531DCF6CC CRC64;

Query Match      16.4%; Score 82.5; DB 2; Length 694;
Best Local Similarity 33.3%; Pred. No. 61;
Matches 33; Conservativity 11; Mismatches 42; Indels 13; Gaps 4;

QY      3 LALLGCVLSCSSAAAFVGS-APVAPQVVALESAAEAGTIANPLGTLP-----L 57
      438 MVPLFISEMDAGAAAFGMAAEPOAPVDT--SAAAGAG-----GHVTPDEAEA 489
      490 KARLIRAGLVPVPGERAGNAVBAVISMSALGFPVALKAL 528

Db

QY      58 KLLLSLGIIPVNHILIEGSKVAELGPOAVGAVKALKAL 96
      490 KARLIRAGLVPVPGERAGNAVBAVISMSALGFPVALKAL 528

Db

RESULT 14
QY      ID Q6H4X3      PRELIMINARY;      PRT;      117 AA.
AC      Q6H4X3;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Hypothetical protein OSJNBa0085X2.14 (Hypothetical protein
DE      OSJNBa0023117.30).
GN      Name=OSJNBa0085X2.14; Synonyms=OSJNBa0023117.30;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Katayose Y.;
RL      Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Yamamoto K.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AP005804; BAD26226.1; -.
DR      EMBL: AP004863; BAD25557.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 117 AA; 11719 MW; 2A7303E30D68D0ED CRC64;

Query Match      16.3%; Score 82; DB 2; Length 117;
Best Local Similarity 32.9%; Pred. No. 14;
Matches 26; Conservativity 9; Mismatches 34; Indels 10; Gaps 2;

QY      6 LIGLCVALLSCSSAAAFVGSAXPVAPVVALESAAEAGTIANPLGT-----PLGT-----LN 55
      6 LIGLCVALLSCSSAAAFVGSAXPVAPVVALESAAEAGTIANPLGT-----PLGT-----LN 55

```

Db 17 LLSCAVAAASHHTAAAAEAGSTSPPAAPQLGMPRSATACGMRGTGRREYYPGTGLPSFQLP 76
 QY 56 PLKLLLSLIGIPVNHILIEG 74
 Db 77 PIVQFPPTLPVPPGMAAG 95

RESULT 15

062CF0 PRELIMINARY; PRT; 540 AA.
 ID 062CF0
 AC 062CF0
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE di-haem cytochrome c peroxidase family protein.
 GN ORFNames=BMAA0945;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Niernman W.C., Deshazer D., Kim H.S., Tetteijn H., Nelson K.E.,
 RA Feidbylum T., Ulrich R.L., Roming C.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarría S.,
 RA Selengut J., Shamblyn C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the Burkholderia mallei genome."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000011; AAU46131.1; -.
 KW Peroxidase.
 SQ SEQUENCE 540 AA; 57096 MM; 298E2A368B38ED9 CRC64;

Query Match 16.3%; Score 82; DB 2; Length 540;
 Best Local Similarity 32.0%; Pred. No. 54;
 Matches 31; Conservative 12; Mismatches 34; Indels 20; Gaps 5;

QY 14 SCSAAAFVLSAKP-----VAQPVAALESAAEAGTLAN--PL-----GTINPLK 58
 Db 55 ACASATAFASGAAAFGALDAVRAHYPASSLSPTFTPGAGAAHVQEAALRAKAASPS 114
 QY 59 LLLSLIGIPVNHILIEG--QKVAELG---PQAVGAV 90
 Db 115 SLTPSPSPPTTSLPGAPQGRVAVATIGRTGPQVASKV 151

Search completed: March 5, 2005, 21:27:23
 Job time : 224 secs

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: March 5, 2005, 21:19:54 ; Search time 163 Seconds
(without alignments) 246.767 Million cell updates/sec

Title: US-09-989-731-408
Sequence: 1 MKLAALLGLCVALLSCSSAAA.....QAVGAVKALKALLGALTVEG 104
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
2105692 segs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV65757	standard;	protein;	104	AA.	
DE	Membrane-bound protein					PRO1245.
PN	WO9630088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 2						
ID	AAV44458	standard;	protein;	104	AA.	
DE	Human lung specific gene protein					Ing107.
PN	WO960160-A1.					
PD	25-NOV-1999.					
PA	(DIAD-) DIADEXUS LLC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 3						
ID	AAV87288	standard;	protein;	104	AA.	
DE	Human signal peptide containing protein					HSP-65 SEQ ID NO:65.
PN	WO20000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 4						
ID	AAV65280	standard;	protein;	104	AA.	
DE	Human PRO1245 (UNO629) protein					sequence SEQ ID NO:408.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 4;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 5						
ID	AAV86141	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	WO200153486-A1.					
PD	26-JUL-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 5;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 6						
ID	ABU58095	standard;	protein;	104	AA.	

DE	Human PRO polypeptide	#127.				
PN	US2003027163-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 7						
ID	ABU59173	standard;	protein;	104	AA.	
DE	Novel human secreted or transmembrane protein					PRO1245.
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 8						
ID	ABU82685	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein					PRO1245.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 9						
ID	AAO19895	standard;	protein;	104	AA.	
DE	Human uteroglobin related protein					2.
PN	WO2003000111-A2.					
PD	03-JAN-2003.					
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 10						
ID	ABU60604	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 11						
ID	ABU13986	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH) GENENTECH LTD.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 12						
ID	ABU72571	standard;	protein;	104	AA.	
DE	Novel human secreted and transmembrane protein					PRO1245.
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 13						
ID	ABU59120	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 14						
ID	ABO26017	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 15						
ID	ABU59026	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2002142961-A1.					
PD	03-OCT-2002.					
PA	(GETH) GENENTECH INC.					

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Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 16
ID ABU92404 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 17
ID ABUS9469 standard; protein; 104 AA.
DE Novel human secreted or transmembrane protein PRO1358.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 18
ID ABUS92235 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 19
ID ABU10941 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GENTH ) GENEINTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 20
ID ABU81693 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GENTH ) GENEINTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 21
ID ABUS8632 standard; protein; 104 AA.
DE Human secreted and transmembrane polypeptide PRO1245.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GENTH ) GENEINTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 22
ID ABO34146 standard; protein; 104 AA.
DE Human PRO1245 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 23
ID ADA37919 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GENTH ) GENEINTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 24
ID ADA21605 standard; protein; 104 AA.
DE Human secreted/transmembrane polypeptide PRO1245.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 25
ID ADA10392 standard; protein; 104 AA.
DE Human secreted/transmembrane protein, PRO1245.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 26
ID ADA17936 standard; protein; 104 AA.
DE Human PRO1245 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 27
ID ADA28044 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 28
ID ADA94624 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 29
ID ADA38849 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 30
ID ADA2970 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
RESULT 31
ID ABO53232 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
RESULT 32
ID ADA2531 standard; protein; 104 AA.
DE Human secreted/transmembrane polypeptide PRO1245.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
RESULT 33
ID ABO22602 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
RESULT 34
ID ADA0697 standard; protein; 104 AA.
DE Human secreted/transmembrane PRO polypeptide #127.
PN US2003049658-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
RESULT 35
ID ADA39390 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
```


RESULT 36
ID ADB96416 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 37
ID ADC57888 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 38
ID ADC53522 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 39
ID ADC12119 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 40
ID ADC56541 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 41
ID ADC56541 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 42
ID ADC07596 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 43
ID ADC1586 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 44
ID ADC14708 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 45
ID ADC82065 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 46
ID ADD07707 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.

PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 47
ID ADC82598 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 48
ID ADD08778 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 49
ID ADD07027 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 50
ID ADC83274 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 51
ID ADD55381 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 52
ID ADD56339 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 53
ID ADD54777 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 54
ID ADE26931 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 55
ID ADE26398 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;
Pred. No. 2e-48;
RESULT 56
ID ADF67335 standard; protein; 104 AA.
DE Human PRO1245 amino acid sequence SEQ ID NO:408.

PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 57
ID ADI35589 standard; protein; 104 AA.
DE Human PRO polypeptide #127.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 58
ID ADJ37309 standard; protein; 104 AA.
DE Human tumour therapy associated PRO1245.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 59
ID ADI00082 standard; protein; 104 AA.
DE Novel human secreted and transmembrane protein PRO1245.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 60
ID ADF35534 standard; protein; 104 AA.
DE Human PRO1245 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 61
ID ADG11784 standard; protein; 104 AA.
DE Human PRO1245 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 62
ID ADH19654 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 63
ID ADG68233 standard; protein; 104 AA.
DE Human PRO polypeptide #14.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 64
ID ADH21147 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 65
ID ADH20187 standard; protein; 104 AA.
DE Human secreted/transmembrane protein PRO1245.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;

RESULT 66
ID ADP07777 standard; protein; 104 AA.
DE Human secreted protein, seq id 260.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 502; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-48;
RESULT 67
ID AAW5868 standard; protein; 104 AA.
DE IUI05 polypeptide sequence.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 99.2%; Score 498; DB 2; Length 104;
Best Local Similarity 99.0%; Pred. No. 5.6e-48;
RESULT 68
ID ADI36315 standard; protein; 104 AA.
DE Full-length hTIN-1 polypeptide, seq id 1.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 99.0%; Score 497; DB 7; Length 104;
Best Local Similarity 99.0%; Pred. No. 7.2e-48;
RESULT 69
ID ADU75657 standard; protein; 104 AA.
DE Marker gene related amino acid sequence SEQ ID NO.909.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 99.0%; Score 497; DB 8; Length 104;
Best Local Similarity 99.0%; Pred. No. 7.2e-48;
RESULT 70
ID ADI36316 standard; protein; 86 AA.
DE Mature hTIN-1 polypeptide, seq id 2.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 82.1%; Score 412; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.1e-38;
RESULT 71
ID ADI36317 standard; protein; 84 AA.
DE Mature hTIN-1 polypeptide, seq id 22.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 81.3%; Score 408; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.7e-38;
RESULT 72
ID AAO19693 standard; protein; 104 AA.
DE Murine uteroglobin related protein 2.
PN WO2003000111-A2.
PD 03-JAN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 49.8%; Score 250; DB 6; Length 104;
Best Local Similarity 57.0%; Pred. No. 4.6e-20;
RESULT 73
ID ADI36321 standard; protein; 104 AA.
DE Full-length hTIN-1 polypeptide, seq id 5.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 49.8%; Score 250; DB 7; Length 104;
Best Local Similarity 57.0%; Pred. No. 4.6e-20;
RESULT 74
ID ADI36326 standard; peptide; 93 AA.
DE Full-length hTIN-1 polypeptide, seq id 21.
PN WO200268673-A2.
PD 06-SEP-2002.

PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 46.2%; Score 232; DB 7; Length 93;
Best Local Similarity 57.1%; Pred. No. 4.2e-18;
RESULT 75
ID ADI36328 standard; peptide; 83 AA.
DE Mature rHIN-1 polypeptide; seq id 27.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.9%; Score 225.5; DB 7; Length 83;
Best Local Similarity 60.5%; Pred. No. 2e-17;
RESULT 76
ID ADI36322 standard; protein; 85 AA.
DE Mature rHIN-1 polypeptide; seq id 6.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.0%; Score 221; DB 7; Length 85;
Best Local Similarity 57.5%; Pred. No. 6.5e-17;
RESULT 77
ID ADI36323 standard; protein; 83 AA.
DE Mature rHIN-1 polypeptide; seq id 24.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 43.6%; Score 219; DB 7; Length 83;
Best Local Similarity 57.6%; Pred. No. 1.1e-16;
RESULT 78
ID AAM62068 standard; protein; 93 AA.
DE Human lung tissue gene LUI03 protein.
PN WO9820143-A1.
PD 14-MAY-1998.
PA (ABRO) ABBOTT LAB.
Query Match 31.9%; Score 160; DB 2; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 79
ID AAY28334 standard; protein; 93 AA.
DE LUI03 specific amino acid consensus sequence.
PN US5939285-A.
PD 17-AUG-1999.
PA (ABRO) ABBOTT LAB.
Query Match 31.9%; Score 160; DB 2; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 80
ID AAY44456 standard; protein; 93 AA.
DE Human lung specific gene protein Lng101.
PN WO9960160-A1.
PD 25-NOV-1999.
PA (DIAD-) DIADEXUS LLC.
Query Match 31.9%; Score 160; DB 3; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 81
ID AAY87289 standard; protein; 93 AA.
DE Human signal peptide containing protein HSP-66 SEQ ID NO:66.
PN WO200000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 31.9%; Score 160; DB 3; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 82
ID AAU29145 standard; protein; 93 AA.
DE Human PRO polypeptide sequence #122.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GENT) GENENTECH INC.
Query Match 31.9%; Score 160; DB 4; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 83
ID ABUS8521 standard; protein; 93 AA.

DE Human PRO polypeptide #122.
PN US20030327272-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 84
ID ABUS8069 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 85
ID ABUS4384 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 86
ID ABR66258 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 87
ID ABR65648 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 88
ID ABUS9588 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 89
ID ABUS2827 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 90
ID ABUS9948 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 91
ID ABR68197 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 92
ID AAO19894 standard; protein; 93 AA.
DE Human uteroglobin related protein 1.
PN WO2003000111-A2.
PD 03-JAN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 93
ID ABUS6250 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036144-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 94

ID ABU92681 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036149-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 95

ID ABO08758 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003044923-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 96

ID ABO02810 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003040062-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 97

ID ABR74964 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040056-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 98

ID ABR94726 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003044926-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 99

ID ABU85699 standard; protein; 93 AA.

DE Human PRO polypeptide #122.

PN US2003036140-A1.

PD 20-FEB-2003.

Query Match

PA (GETH) GENENTECH INC.

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 100

ID ABU98859 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003013153-A1.

PD 16-JAN-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 101

ID ABU98074 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003017544-A1.

PD 23-JAN-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 102

ID ABU91780 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003027277-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 103

ID ABU89473 standard; protein; 93 AA.

DE Human PRO polypeptide #122.

PN US2003036141-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
PD 13-FEB-2003.Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 104

ID ABU86314 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036146-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 105

ID ABU67527 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036162-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 106

ID ABU80555 standard; protein; 93 AA.

DE Human PRO protein #122.

PN US2003036137-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 107

ID ABR9473 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040063-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 108

ID ABR98863 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040064-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 109

ID ABO16386 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003027267-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 110

ID ABR92286 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003036160-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 111

ID ABO16927 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003044925-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 112

ID ABR78348 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003054474-A1.

PD 20-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 113

ID ABU85084 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003032114-A1.

PD 13-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
PD 13-FEB-2003.

Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 114
ID ABO00223 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 115
ID ABO11555 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 116
ID ABO02200 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 117
ID ABU88774 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 118
ID ABU83469 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 119
ID ABO06270 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 120
ID ABR5306 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 121
ID ABO09368 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 122
ID ABO19232 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036118-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 123
ID ABO11250 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 124
ID ABR66868 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 125
ID ABO16081 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 126
ID ABO13787 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 127
ID ABU65690 standard; protein; 93 AA.
DE Human secreted/transmembrane protein, SEQ ID 244.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 128
ID ABO07538 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 129
ID ABO03725 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 130
ID ABR67173 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027286-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 131
ID ABO15776 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054483-A1.
PD 20-MAR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 132
ID ABUS6057 standard; protein; 93 AA.
DE Human secreted/transmembrane protein, PRO1128.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 133
ID ABUS6385 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 134
ID ABUS5330 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 135 43.6%; Pred. No. 5.4e-10;
ID ABR71233 standard; protein; 93 AA.
DE Human PRO1128 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 136 43.6%; Pred. No. 5.4e-10;
ID ABO07843 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 137 43.6%; Pred. No. 5.4e-10;
ID ABR70084 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032138-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 138 43.6%; Pred. No. 5.4e-10;
ID ABR69417 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 139 43.6%; Pred. No. 5.4e-10;
ID ABO01558 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 140 43.6%; Pred. No. 5.4e-10;
ID ABR61360 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 141 43.6%; Pred. No. 5.4e-10;
ID ABR60157 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 142 43.6%; Pred. No. 5.4e-10;
ID ABR67892 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 143 43.6%; Pred. No. 5.4e-10;
ID ABR65280 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 144 43.6%; Pred. No. 5.4e-10;
ID ABR6502 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027271-A1.

PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 145 43.6%; Pred. No. 5.4e-10;
ID ABR71914 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 146 43.6%; Pred. No. 5.4e-10;
ID ABR65394 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 147 43.6%; Pred. No. 5.4e-10;
ID ABR89084 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 148 43.6%; Pred. No. 5.4e-10;
ID ABR63164 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 149 43.6%; Pred. No. 5.4e-10;
ID ABR95020 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 150 43.6%; Pred. No. 5.4e-10;
ID ABR90568 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 151 43.6%; Pred. No. 5.4e-10;
ID ABR84079 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 152 43.6%; Pred. No. 5.4e-10;
ID ABR93730 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 153 43.6%; Pred. No. 5.4e-10;
ID ABR64975 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 154 43.6%; Pred. No. 5.4e-10;
ID ABR68807 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027271-A1.

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PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 155
ID ABO06623 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 156
ID ABR99168 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 157
ID ABU57052 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 158
ID ABU86004 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 159
ID ABU82291 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 160
ID ABU87302 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 161
ID ABU83774 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 162
ID ABO08148 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 163
ID ABU81859 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 164
ID ABU66023 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 165
ID ABR59852 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 166
ID ABU94040 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 167
ID ABU9893 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 168
ID ABR66563 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 169
ID ABR90981 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 170
ID ABU94408 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 171
ID ABU79290 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 172
ID ABU86619 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 173
ID ABU8924 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 174
ID ABU94713 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 175
ID ABO04640 standard; protein; 93 AA.
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DE Human PRO polypeptide #122.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 176
ID ABR70389 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 177
ID ABR98854 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 178
ID ABR65953 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
PA (GETH ) GENENTECH INC.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 179
ID ABR64670 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 180
ID ABR79595 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 181
ID ABR92986 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 182
ID ABR95945 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 183
ID ABR91165 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 184
ID ABR90258 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 185
ID ABO09673 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 186
ID ABO10945 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 187
ID ABR70999 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 188
ID ABR87607 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 189
ID ABR91475 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 190
ID ABR84689 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 191
ID ABR69779 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 192
ID ABR80156 standard; protein; 93 AA.
DE Human PRO protein #122.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 193
ID ABR93425 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 194
ID ABO09978 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
RESULT 195
ID ABO09063 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
  31.9%; Score 160; DB 6; Length 93;
  43.6%; Pred. No. 5.4e-10;
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RESULT 196
ID ABU10631 standard; protein; 93 AA.
DE Human secreted/transmembrane protein #122.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 197
ID ABU95640 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 198
ID ABU96849 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 199
ID ABR70694 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 200
ID ABO05045 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 201
ID ABO08453 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 202
ID ABO05660 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 203
ID ABR74049 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 204
ID ABR95641 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 205
ID ABR80938 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 206
ID ABR81243 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 207
ID ABM00939 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 208
ID ABR88541 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 209
ID ABM77362 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 210
ID ABO28846 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 211
ID ABO31591 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 212
ID ABM08008 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 213
ID ABO40488 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 214
ID ABO35913 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;

Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 215
ID ABO44052 standard; protein: 93 AA.
DE Human PRO polypeptide #122.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 216
ID ADA77996 standard; protein: 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 217
ID ABR24847 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 218
ID ABO03115 standard; protein: 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 219
ID ABR90371 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 220
ID ABM17285 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 221
ID ABR95031 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 222
ID ABR95336 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 223
ID ABO21574 standard; protein: 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 224
ID ABR97838 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064452-A1.
PA (GETH) GENENTECH INC.

03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 225
ID ABR87626 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 226
ID ABR77667 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 227
ID ABR27897 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 228
ID ABM06178 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 229
ID ABM03684 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 230
ID ABM35135 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 231
ID ABM26372 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 232
ID ABO48154 standard; protein: 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 233
ID ABR92896 standard; protein: 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 234
ID ABO43747 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068732-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 235
ID ABM1668 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064447-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 236
ID ABM02769 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073184-AL.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 237
ID ABM16065 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064463-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 238
ID ABO27626 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064451-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 239
ID ABM29117 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068721-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 240
ID ABM07093 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068699-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 241
ID ABM2187 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068707-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 242
ID ABM09533 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073175-AL.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;

Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 243
ID ABO41403 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068695-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 244
ID ABO36218 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068703-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 245
ID ABO43747 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068732-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 246
ID ABM76447 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003082717-AL.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 247
ID ABM76143 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104548-AL.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 248
ID ABM25762 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104542-AL.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 249
ID ABM26067 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104543-AL.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 250
ID ABO03420 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036127-AL.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 251
ID ABO02505 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040061-AL.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 252
ID ABR9676 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036130-AL.
PD 20-FEB-2003.

Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 253
ID ABR73744 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 254
ID ABO16996 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 255
ID ABR94421 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 256
ID ABR75928 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 257
ID ABR71304 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 258
ID ABR93201 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 259
ID ABR93506 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 260
ID ABR87931 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 261
ID ABO27931 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 262

ID ABO30066 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 263
ID ABO33275 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 264
ID ABO4963 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 265
ID ABO8923 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 266
ID ABO36523 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 267
ID ABO35608 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 268
ID ABO39573 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 269
ID ABO10448 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 270
ID ABO11973 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 271
ID ABO52119 standard; protein; 93 AA.

DE Human PRO polypeptide #122.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 272
ID ABO52424 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 273
ID ABO23742 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 274
ID ABR97228 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 275
ID ABR87016 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 276
ID ABM1058 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 277
ID ABM28202 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 278
ID ABO32201 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 279
ID ABM15328 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 280
ID ABM06483 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068709-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 281
ID ABM04294 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 282
ID ABM22407 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 283
ID ABM07703 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 284
ID ABO40793 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 285
ID ABM35440 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 286
ID ABM33203 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 287
ID ABO52729 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 288
ID ABO50289 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 289
ID ABU9283 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;

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Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 290
ID ABO04335 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 291
ID ABO05965 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 292
ID ABO18505 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 293
ID ABR9753 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 294
ID ABR8063 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 295
ID ABO0124 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 296
ID ABR8884 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 297
ID ABO1349 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 298
ID ABO2088 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 299
ID ABO4203 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 300
ID ABO4262 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 301
ID ABO1014 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 302
ID ABO3865 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 303
ID ABO3289 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 304
ID ABO2272 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 305
ID ABO7492 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 306
ID ADA7978 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 307
ID ABR6313 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 308
ID ABO2464 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
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RESULT 309
ID ABR86406 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 310
ID ABR86711 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 311
ID ABR16675 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 312
ID ABR29727 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 313
ID ABO29151 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 314
ID ABR23932 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 315
ID ABR23322 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 316
ID ABR22102 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 317
ID ABO37743 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 318

ID ABR28507 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 319
ID ABR28812 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 320
ID ABR66456 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003088737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 321
ID ABR75838 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 322
ID ABR3418 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 323
ID ABR34423 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 324
ID ABO20354 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 325
ID ABO21269 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 326
ID ABO22184 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 327
ID ABR96618 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 328
ID ABR85796 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 329
ID ABR9778 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 330
ID ABM00329 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 331
ID ABM00634 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 332
ID ABO29761 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 333
ID ABM23627 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 334
ID ABM29422 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 335
ID ABO38353 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 336
ID ABO45653 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 337
ID ABR89761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 338
ID ABR81548 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003048744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 339
ID ABO16691 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 340
ID ABO18317 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 341
ID ABO22744 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003027255-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 342
ID ABO23049 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 343
ID ABR92591 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 344
ID ABR81548 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003048744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 345
ID ABM77972 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 346
ID ABR89761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 347
ID ABM26677 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 348
ID ABM13803 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 349
ID ABO28541 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 350
ID ABO30371 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 351
ID ABM07398 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 352
ID ABM03989 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 353
ID ABO37133 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 354
ID ABO41708 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 355
ID ABO35303 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 356
ID AM25152 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 357
ID ABO47544 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 358
ID ABO47849 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 359
ID ABO48459 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 360
ID ABO51509 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 361
ID ABO51814 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 362
ID ABO50594 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003048779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 363
ID ABR79718 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 364
ID ABM16980 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 365
ID ABO18012 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.

[illegible]

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RESULT 375
ID ABO39268 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
FN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 376
ID ABM75533 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 377
ID ABM25457 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 378
ID ABM19667 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 379
ID ABO46873 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
FN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 380
ID ABO47178 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
FN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 381
ID ADA83313 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
FN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 382
ID ABR71609 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 383
ID ABR72219 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 384
ID ABR8558 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
FN US2003036129-A1.

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PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 385
ID ABO06928 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 386
ID ABR84881 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 387
ID ABR73439 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 388
ID ABR7653 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 389
ID ABR7134 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 390
ID ABM18200 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 391
ID ABO20659 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 392
ID ABO25402 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 393
ID ABO25707 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 394
ID ABR94116 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 395
ID ABR80023 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 396
ID ABM11363 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 397
ID ABO32970 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 398
ID ABO30676 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 399
ID ABO30981 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 400
ID ABM27287 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 401
ID ABM30032 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 402
ID ABM05568 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 403
ID ABM15633 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068698-A1.
PD 10-APR-2003.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 404
ID ABM08618 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 405
ID ABO42318 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 406
ID ABO38048 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 407
ID ABO45958 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 408
ID ABM66761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 409
ID ADB20356 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 410
ID ABM19662 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 411
ID ABO49374 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 412
ID ABO49679 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 413
ID ADA78608 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 414
ID ABR88236 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 415
ID ABM26982 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 416
ID ABM03379 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 417
ID ABO39878 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 418
ID ABO49984 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 419
ID ABO50899 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 420
ID ABO05355 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 421
ID ABR74659 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 422
ID ABR77138 standard; protein; 93 AA.
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DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US200304927-A1.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 423
ID ABM17895 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 424
ID ABR95946 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 425
ID ABO21879 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 426
ID ABO20049 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 427
ID ABO24352 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 428
ID ABR6101 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 429
ID ABM10753 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 430
ID ABM76752 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 431
ID ABR9456 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 432
ID ABM12583 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 433
ID ABM05873 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 434
ID ABO3498 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 435
ID ABM03074 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 436
ID ABM19052 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 437
ID ABM19357 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 438
ID ABO4656 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 439
ID ABO49069 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 440
ID ABR69112 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003072273-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 441
ID ABR89151 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
ID ABR72524 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 443
ID ABR74354 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 444
ID ABO29651 standard; protein; 93 AA.
DE Human HIN-2 protein.
PN WO2003046125-A2.
PD 05-JUN-2003.
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 445
ID ABO18622 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 446
ID ABR80328 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 447
ID ABO01549 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 448
ID ABO01519 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 449
ID ABR87321 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 450
ID ABR1288 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 451
ID ABR10642 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 452
ID ABR24542 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 453
ID ABO29456 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 454
ID ABO31286 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 455
ID ABR14413 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 456
ID ABO09838 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 457
ID ABO38963 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 458
ID ABR34728 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 459
ID ABO51204 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;

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RESULT 460
ID ABO4030 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-FEB-2003.
RESULT 461
ID ABO10500 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-FEB-2003.
RESULT 462
ID ABR77743 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 27-FEB-2003.
RESULT 463
ID ABR78953 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-MAR-2003.
RESULT 464
ID ABO24047 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054482-A1.
PD 20-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-MAR-2003.
RESULT 465
ID ABR3811 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054457-A1.
PD 20-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 20-MAR-2003.
RESULT 466
ID ABM01854 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059883-A1.
PD 27-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 27-MAR-2003.
RESULT 467
ID ABM78277 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049764-A1.
PD 13-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 13-MAR-2003.
RESULT 468
ID ABR90066 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073177-A1.
PD 17-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 17-APR-2003.
RESULT 469
ID ABM27592 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 03-APR-2003.
RESULT 470
ID ABM3193 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064450-A1.
PD 03-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 03-APR-2003.
RESULT 471
ID ABO31896 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068731-A1.
PD 10-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
RESULT 472
ID ABM14108 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
RESULT 473
ID ABM08313 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
RESULT 474
ID ABO40183 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 10-APR-2003.
RESULT 475
ID ABM74618 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096351-A1.
PD 22-MAY-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 22-MAY-2003.
RESULT 476
ID ABM3813 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 22-MAY-2003.
RESULT 477
ID ABM20272 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104556-A1.
PD 05-JUN-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 05-JUN-2003.
RESULT 478
ID ABO48764 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049756-A1.
PD 13-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  PD 13-MAR-2003.
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RESULT 479
ID ABR72829 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 480
ID ABO15471 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 481
ID ABR85186 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 482
ID ABO15166 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 483
ID ABO17301 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 484
ID ABO17590 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 485
ID ABR85491 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 486
ID ABO77057 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 487
ID ABO28236 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 488
ID ABM23017 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 489
ID ABM30337 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 490
ID ABM21797 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 491
ID ABM21492 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 492
ID ABM15023 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 493
ID ABO41098 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 494
ID ABO36828 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 495
ID ABO37438 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 496
ID ABM75228 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
RESULT 497
ID ABM33508 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
Pred. No. 5.4e-10;
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Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 498
ID ABO4623 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 499
ID ADA82679 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 500
ID ABM31862 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 501
ID ABM31252 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 502
ID ADB85987 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 503
ID ABM32167 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 504
ID ABM32472 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 505
ID ABM31557 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 506
ID ABM30947 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 507

ID ADD05717 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 508
ID ADG02712 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 509
ID ADG01419 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 510
ID ADF95594 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 511
ID ADG12409 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 512
ID ADH09069 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 513
ID ADL32850 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 514
ID ADM30384 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 515
ID ADN39907 standard; protein; 93 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C277.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSH-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;
RESULT 516
ID ADE74381 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.

PN US2003211572-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
ID ADE74993 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 518
ID ADP6206 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 519
ID ADG04477 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 520
ID ADG00637 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 521
ID ADG82893 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 522
ID ADH26174 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 523
ID ADH33143 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 524
ID ADJ54882 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 525
ID ADJ64653 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
31.9%; Score 160; DB 8; Length 93;
PD (USSH) US DEPT HEALTH & HUMAN SERVICES.

Best Local Similarity 43.6%; Pred. No. 5.4e-10;
ID ADM31549 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 527
ID ADM36596 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 528
ID ADJ40401 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 529
ID ADN38009 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;
RESULT 530
ID ADO78100 standard; protein; 93 AA.
DE Human SCGB3A2.
PN DE10254601-A1.
PD 03-JUN-2004.
PA (GANV-) GANNVED PHARM AG.
Query Match
Best Local Similarity 30.1%; Score 151; DB 8; Length 93;
RESULT 531
ID AAU14471 standard; protein; 87 AA.
DE Human novel protein #342.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 28.9%; Score 145; DB 4; Length 87;
RESULT 532
ID ADH80789 standard; protein; 87 AA.
DE Human polypeptide #106.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG-) TANG Y T.
PA (LIUC-) LITU C.
PA (ASUN-) ASDUDI V.
PA (CHEN-) CHEN R.
PA (QIAN-) QIAN X B.
PA (WANG-) WANG Z W.
PA (WEHR-) WEHRMAN T.
PA (ZHAN-) ZHANG J.
PA (ZHOU-) ZHOU P.
PA (CAOY-) CAO Y.
PA (DRMA/) DRMANC R T.
Query Match
Best Local Similarity 28.9%; Score 145; DB 8; Length 87;
RESULT 533
ID AAO19892 standard; protein; 91 AA.
DE Murine uteroglobin related protein 1 type A.
PN WO2003000111-A2.
PD 03-JAN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query Match 26.9%; Score 135; DB 6; Length 91;
Best Local Similarity 36.0%; Pred. No. 3.4e-07;
RESULT 534
ID AAO29652 standard; protein; 91 AA.
DE Mouse HTN-2 protein.
PN W02003046125-A2.
PD 05-JUN-2003.
PA (NAJB-) NAT JEWISH MEDICAL & RES CENT.
Query Match 26.9%; Score 135; DB 7; Length 91;
Best Local Similarity 36.0%; Pred. No. 3.4e-07;
RESULT 535
ID AD136329 standard; peptide; 93 AA.
DE Human UGRF-1 polypeptide, seq id 32.
PN W0200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 26.9%; Score 135; DB 7; Length 93;
Best Local Similarity 40.6%; Pred. No. 3.5e-07;
RESULT 536
ID AAU14235 standard; protein; 137 AA.
DE Human novel protein #106.
PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSBQ INC.
Query Match 26.9%; Score 135; DB 4; Length 137;
Best Local Similarity 41.9%; Pred. No. 5.8e-07;
RESULT 537
ID AAU75869 standard; protein; 26 AA.
DE LUI105 polypeptide derived peptide sequence 1.
PN W09833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 23.5%; Score 118; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
RESULT 538
ID AAU75871 standard; protein; 21 AA.
DE LUI105 polypeptide derived peptide sequence 3.
PN W09833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 19.9%; Score 100; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00043;
RESULT 539
ID AAU75870 standard; protein; 19 AA.
DE LUI105 polypeptide derived peptide sequence 2.
PN W09833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 18.3%; Score 92; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.003;
RESULT 540
ID AAU75872 standard; protein; 18 AA.
DE LUI105 polypeptide derived peptide sequence 4.
PN W09833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 17.7%; Score 89; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0061;
RESULT 541
ID AAU75873 standard; protein; 19 AA.
DE LUI105 polypeptide derived peptide sequence 5.
PN W09833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 16.5%; Score 83; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.031;
RESULT 542
ID AAU44403 standard; protein; 673 AA.
DE Human truncated tankyrase-1.
PN W0964606-A1.
PD 16-DEC-1999.
PA (UYRQ) UNIV ROCKEFELLER.

Query Match 16.5%; Score 83; DB 3; Length 673;
Best Local Similarity 30.5%; Pred. No. 3.4;
RESULT 543
ID AAU79538 standard; protein; 673 AA.
DE Truncated human tankyrase #1.
PN W0200229017-A2.
PD 11-APR-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 16.5%; Score 83; DB 5; Length 673;
Best Local Similarity 30.5%; Pred. No. 3.4;
RESULT 544
ID AAU44404 standard; protein; 949 AA.
DE Human truncated tankyrase-2.
PN W0964606-A1.
PD 16-DEC-1999.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 16.5%; Score 83; DB 3; Length 949;
Best Local Similarity 30.5%; Pred. No. 5.3;
RESULT 545
ID AAU79539 standard; protein; 949 AA.
DE Truncated human tankyrase #2.
PN W0200229017-A2.
PD 11-APR-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 16.5%; Score 83; DB 5; Length 949;
Best Local Similarity 30.5%; Pred. No. 5.3;
RESULT 546
ID AAU44402 standard; protein; 1327 AA.
DE Human tankyrase.
PN W0964606-A1.
PD 16-DEC-1999.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 16.5%; Score 83; DB 3; Length 1327;
Best Local Similarity 30.5%; Pred. No. 8.3;
RESULT 547
ID AAB27212 standard; protein; 1327 AA.
DE Human tankyrase I protein sequence SEQ ID NO: 8.
PN W0200061813-A1.
PD 19-OCT-2000.
PA (GERO-) GERON CORP.
Query Match 16.5%; Score 83; DB 4; Length 1327;
Best Local Similarity 30.5%; Pred. No. 8.3;
RESULT 548
ID AAB66279 standard; protein; 1327 AA.
DE Human tankyrase1 SEQ ID NO: 4.
PN W0200100849-A1.
PD 04-JAN-2001.
PA (ICOS-) ICOS CORP.
Query Match 16.5%; Score 83; DB 4; Length 1327;
Best Local Similarity 30.5%; Pred. No. 8.3;
RESULT 549
ID AAU79537 standard; protein; 1327 AA.
DE Human tankyrase.
PN W0200229017-A2.
PD 11-APR-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 16.5%; Score 83; DB 5; Length 1327;
Best Local Similarity 30.5%; Pred. No. 8.3;
RESULT 550
ID ADR14791 standard; protein; 1327 AA.
DE Amino acid sequence of human MAPCAX orthologue #23.
PN W02004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 16.5%; Score 83; DB 8; Length 1327;
Best Local Similarity 30.5%; Pred. No. 8.3;
RESULT 551
ID ABO76950 standard; protein; 718 AA.
DE Pseudomonas aeruginosa polypeptide #9125.
PN U86551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 16.4%; Score 82.5; DB 7; Length 718;

Best Local Similarity 37.3%; Pred. No. 4.2;
RESULT 552
ID ABR63120 standard; protein: 439 AA.
DE Penicillium lypc1i phytaase.
PN WO2003062409-A2.
PD 31-JUL-2003.
PA (HOPE) ROCHE VITAMINS AG.
Query Match 15.8%; Score 79.5; DB 7; Length 439;
Best Local Similarity 29.9%; Pred. No. 4.6;
RESULT 553
ID ABO73010 standard; protein: 255 AA.
DE Pseudomonas aeruginosa polypeptide #5185.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.6%; Score 78.5; DB 7; Length 255;
Best Local Similarity 24.1%; Pred. No. 3;
RESULT 554
ID ABO80397 standard; protein: 540 AA.
DE Pseudomonas aeruginosa polypeptide #12572.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.3%; Score 77; DB 7; Length 540;
Best Local Similarity 30.0%; Pred. No. 12;
RESULT 555
ID ABU22766 standard; protein: 561 AA.
DE Protein encoded by Prokaryotic essential gene #8293.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 15.1%; Score 76; DB 6; Length 561;
Best Local Similarity 26.4%; Pred. No. 16;
RESULT 556
ID ABP66002 standard; protein: 889 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:746.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 15.1%; Score 76; DB 5; Length 889;
Best Local Similarity 25.7%; Pred. No. 30;
RESULT 557
ID ABP66269 standard; protein: 496 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1013.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 15.0%; Score 75.5; DB 5; Length 496;
Best Local Similarity 30.3%; Pred. No. 16;
RESULT 558
ID ADS21025 standard; protein: 855 AA.
DE Bacterial polypeptide #10058.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
DE (HINK/) HINKLE G J.
PN (SLAT/) SLATER S C.
PD (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 15.0%; Score 75.5; DB 8; Length 855;
Best Local Similarity 32.9%; Pred. No. 32;
RESULT 559
ID AAB42153 standard; protein: 361 AA.
DE Human ORFX ORF1917 polypeptide sequence SEQ ID NO:3834.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 75; DB 3; Length 361;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 560
ID ADN99707 standard; protein: 362 AA.
DE Novel human protein sequence #523.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 561
ID ADO20269 standard; protein: 362 AA.
DE Human PRO polypeptide #585.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 562
ID AEM81662 standard; protein: 362 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82491, SEQ:4297.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 563
ID AAM68511 standard; protein: 469 AA.
DE B. flavum fumase protein.
PN JP10262684-A.
PD 06-OCT-1998.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 14.7%; Score 74; DB 2; Length 469;
Best Local Similarity 25.0%; Pred. No. 22;
RESULT 564
ID AAB76752 standard; protein: 358 AA.
DE Corynebacterium glutamicum MCF protein SEQ ID NO:486.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 14.6%; Score 73.5; DB 4; Length 358;
Best Local Similarity 26.5%; Pred. No. 17;
RESULT 565
ID AAG91541 standard; protein: 358 AA.
DE C glutamicum protein fragment SEQ ID NO: 5295.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOM) KYOMA HAKKO KOGYO KK.
Query Match 14.6%; Score 73.5; DB 4; Length 358;
Best Local Similarity 26.5%; Pred. No. 17;
RESULT 566
ID AAB66866 standard; protein: 443 AA.
DE Human peptidyl-prolyl isomerase-2.
PN US6171843-B1.
PD 09-JAN-2001.
PA (INCY-) INCYTE PHARM INC.
Query Match 14.6%; Score 73.5; DB 4; Length 443;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 567
ID ABU62206 standard; protein: 447 AA.
DE Human peptidyl-prolyl isomerase 2 (HPIP2).
PN US6524838-B1.
PD 25-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 73.5; DB 6; Length 447;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 568
ID ADB87811 standard; protein: 447 AA.
DE Human peptidyl-prolyl isomerase, HPIP-2.
PN US2003087390-A1.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 73.5; DB 7; Length 447;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 569
ID ADC34766 standard; protein: 776 AA.
DE Rat salt inducible kinase seq id 34.
PN US2003087317-A1.
PD 08-MAY-2003.

PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 73.5; DB 7; Length 776;
Best Local Similarity 33.7%; Pred. No. 48;
RESULT 570
ID ADS4317 standard; protein; 739 AA.
DE Bacterial polypeptide #21747.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.5%; Score 73; DB 8; Length 739;
Best Local Similarity 27.1%; Pred. No. 51;
RESULT 571
ID ABB65719 standard; protein; 1279 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23949.
PN MO200171042-A2.
PD 27-SRP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.5%; Score 73; DB 4; Length 1279;
Best Local Similarity 31.6%; Pred. No. 1.1e+02;
RESULT 572
ID AAM49674 standard; protein; 421 AA.
DE T. thermophilus H86 O-acetylhomoserine sulphydase.
PN JP2002010787-A.
PD 15-JAN-2002.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (IKED-) IKEDA SHOKKEN KK.
Query Match 14.4%; Score 72.5; DB 5; Length 421;
Best Local Similarity 37.5%; Pred. No. 28;
RESULT 573
ID AAU42386 standard; protein; 122 AA.
DE Propionibacterium acnes immunogenic protein #3282.
PN MO200181581-A2.
PD 01-NOV-2001.
PA (COR-) CORIXA CORP.
Query Match 14.3%; Score 72; DB 4; Length 122;
Best Local Similarity 39.4%; Pred. No. 6.2;
RESULT 574
ID ABM3905 standard; protein; 122 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3581.
PN MO2003033515-A1.
PD 24-APR-2003.
PA (COR-) CORIXA CORP.
Query Match 14.3%; Score 72; DB 6; Length 122;
Best Local Similarity 39.4%; Pred. No. 6.2;
RESULT 575
ID AAR72643 standard; protein; 236 AA.
DE Leishmania donovani A2 protein of the ORF1 domain.
PN CA2105538-A.
PD 04-MAR-1995.
PA (UYMC-) UNIV MCGILL.
Query Match 14.3%; Score 72; DB 2; Length 236;
Best Local Similarity 29.8%; Pred. No. 15;
RESULT 576
ID AAR71477 standard; protein; 236 AA.
DE Leishmania donovani A2 protein.
PN MO9506729-A1.
PD 09-MAR-1995.
PA (UYMC-) UNIV MCGILL.
Query Match 14.3%; Score 72; DB 2; Length 236;
Best Local Similarity 29.8%; Pred. No. 15;
RESULT 577
ID ADS25292 standard; protein; 395 AA.
DE Bacterial polypeptide #14325.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 579
ID ADS22407 standard; protein; 395 AA.
DE Bacterial polypeptide #11440.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 580
ID ADS25457 standard; protein; 395 AA.
DE Bacterial polypeptide #14490.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 581
ID ABJ04701 standard; protein; 528 AA.
DE Mycobacterium tuberculosis protein 36.
PN MO200244406-A2.
PD 06-JUN-2002.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 14.3%; Score 72; DB 5; Length 528;
Best Local Similarity 28.4%; Pred. No. 43;
RESULT 582
ID ADJ48924 standard; protein; 405 AA.
DE O11-associated gene related protein #424.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDERNAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 14.2%; Score 71.5; DB 8; Length 405;
Best Local Similarity 27.8%; Pred. No. 34;
RESULT 583
ID ADS25947 standard; protein; 432 AA.
DE Bacterial polypeptide #14980.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.2%; Score 71.5; DB 8; Length 432;
Best Local Similarity 26.1%; Pred. No. 37;
RESULT 584
ID ADS25416 standard; protein; 438 AA.

PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 578
ID ADS25842 standard; protein; 395 AA.
DE Bacterial polypeptide #14875.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 579
ID ADS22407 standard; protein; 395 AA.
DE Bacterial polypeptide #11440.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 580
ID ADS25457 standard; protein; 395 AA.
DE Bacterial polypeptide #14490.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 72; DB 8; Length 395;
Best Local Similarity 36.2%; Pred. No. 29;
RESULT 581
ID ABJ04701 standard; protein; 528 AA.
DE Mycobacterium tuberculosis protein 36.
PN MO200244406-A2.
PD 06-JUN-2002.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 14.3%; Score 72; DB 5; Length 528;
Best Local Similarity 28.4%; Pred. No. 43;
RESULT 582
ID ADJ48924 standard; protein; 405 AA.
DE O11-associated gene related protein #424.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDERNAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 14.2%; Score 71.5; DB 8; Length 405;
Best Local Similarity 27.8%; Pred. No. 34;
RESULT 583
ID ADS25947 standard; protein; 432 AA.
DE Bacterial polypeptide #14980.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.2%; Score 71.5; DB 8; Length 432;
Best Local Similarity 26.1%; Pred. No. 37;
RESULT 584
ID ADS25416 standard; protein; 438 AA.

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DE Bacterial polypeptide #14449.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 438;
RESULT 585
ID ADS25098 standard; protein; 450 AA.
DE Bacterial polypeptide #14131.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 450;
RESULT 586
ID ADS22360 standard; protein; 859 AA.
DE Bacterial polypeptide #11393.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 859;
RESULT 587
ID ABG15241 standard; protein; 342 AA.
DE Novel human diagnostic protein #15232.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 14.1%; Score 71; DB 4; Length 342;
RESULT 588
ID ABU22662 standard; protein; 1395 AA.
DE Protein encoded by Prokaryotic essential gene #8189.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 14.1%; Score 71; DB 6; Length 1395;
RESULT 589
ID ADP30057 standard; protein; 578 AA.
DE Human secreted protein SEQ ID #824.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 14.0%; Score 70.5; DB 8; Length 578;
RESULT 590
ID AAM51666 standard; protein; 668 AA.
DE Arabidopsis thaliana heat shock protein like (GenBank: CAB46061).
PN WO200170929-A2.
PD 27-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 14.0%; Score 70.5; DB 4; Length 668;
RESULT 591
ID ADN99804 standard; protein; 902 AA.
DE Novel human protein sequence #620.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
14.0%; Score 70.5; DB 8; Length 902;

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Best Local Similarity	35.0%;	Pred. No. 1.3e+02;
RESULT 592		
ID A0N99803 standard; protein; 902 AA.		
DE Novel human protein sequence #619.		
PN W02004038003-A2.		
PD 06-May-2004.		
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.		
Query Match	14.0%;	Score 70.5; DB 8; Length 902;
Best Local Similarity	35.0%;	Pred. No. 1.3e+02;
RESULT 593		
ID ABU49383 standard; protein; 477 AA.		
DE Protein encoded by Prokaryotic essential gene #34910.		
PN W0200277185-A2.		
PD 03-OCT-2002.		
PA (ELIT-) ELITRA PHARM INC.		
Query Match	13.9%;	Score 70; DB 6; Length 477;
Best Local Similarity	28.1%;	Pred. No. 63;
RESULT 594		
ID ADS23013 standard; protein; 669 AA.		
DE Bacterial polypeptide #12046.		
PN US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Query Match	13.9%;	Score 70; DB 8; Length 669;
Best Local Similarity	27.4%;	Pred. No. 1e+02;
RESULT 595		
ID ABU40129 standard; protein; 362 AA.		
DE Protein encoded by Prokaryotic essential gene #25656.		
PN W0200277183-A2.		
PD 03-OCT-2002.		
PA (ELIT-) ELITRA PHARM INC.		
Query Match	13.8%;	Score 69.5; DB 6; Length 362;
Best Local Similarity	26.0%;	Pred. No. 50;
RESULT 596		
ID AAW73657 standard; protein; 423 AA.		
DE M. tuberculosis antigen clone mTCC#2 protein sequence.		
PN W09853076-A2.		
PD 26-NOV-1998.		
PA (CORI-) CORIXA CORP.		
Query Match	13.8%;	Score 69.5; DB 2; Length 423;
Best Local Similarity	31.8%;	Pred. No. 61;
RESULT 597		
ID AAW7367 standard; protein; 423 AA.		
DE M. tuberculosis antigen clone mTCC#2 protein sequence.		
PN W09853075-A2.		
PD 26-NOV-1998.		
PA (CORI-) CORIXA CORP.		
Query Match	13.8%;	Score 69.5; DB 2; Length 423;
Best Local Similarity	31.8%;	Pred. No. 61;
RESULT 598		
ID AAU08228 standard; protein; 423 AA.		
DE Polypeptide encoded by Mycobacterium tuberculosis clone mTCC#2		
PN W0200162893-A2.		
PD 30-AUG-2001.		
PA (CORI-) CORIXA CORP.		
Query Match	13.8%;	Score 69.5; DB 4; Length 423;
Best Local Similarity	31.8%;	Pred. No. 61;
RESULT 599		
ID AAU01891 standard; protein; 423 AA.		
DE M. tuberculosis antigen mTCC#2 (Mtb011).		
PN W0200124820-A1.		
PD 12-APR-2001.		
PA (CORI-) CORIXA CORP.		
Query Match	13.8%;	Score 69.5; DB 4; Length 423;
Best Local Similarity	31.8%;	Pred. No. 61;
RESULT 600		
ID AAW29715 standard; protein; 423 AA.		
DE Mycobacterium sp. mTCC#1 antigenic protein.		
PN W0200272792-A2.		

PD 19-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 5; Length 423;
Best Local Similarity 31.8%; Pred. No. 61;
RESULT 601
ID AAE17579 standard; protein; 423 AA.
DE Mycobacterium species M7B41 (M7CC #1) protein.
PN W0200198460-A2.
PD 27-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 5; Length 423;
Best Local Similarity 31.8%; Pred. No. 61;
RESULT 602
ID AAB07585 standard; protein; 427 AA.
DE Protein encoded by the bleomycin (BLM) gene cluster ORF31.
PN W0200040704-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 13.8%; Score 69.5; DB 3; Length 427;
Best Local Similarity 32.0%; Pred. No. 62;
RESULT 603
ID AB021223 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #6760.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR) PHARM INC.
Query Match 13.8%; Score 69.5; DB 6; Length 458;
Best Local Similarity 26.5%; Pred. No. 68;
RESULT 604
ID ADL65715 standard; protein; 492 AA.
DE C. glutamicum RXA-associated protein #36.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI) BASF AG.
Query Match 13.8%; Score 69.5; DB 7; Length 492;
Best Local Similarity 29.1%; Pred. No. 74;
RESULT 605
ID AAG90047 standard; protein; 495 AA.
DE C. glutamicum protein fragment SEQ ID NO: 3801.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOM) KYOMA HAKKO KOGYO KK.
Query Match 13.8%; Score 69.5; DB 4; Length 495;
Best Local Similarity 29.1%; Pred. No. 75;
RESULT 606
ID AAY32066 standard; protein; 710 AA.
DE Mycobacterium tuberculosis antigen fusion protein M7B1F.
PN W09951748-A2.
PD 14-OCT-1999.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 2; Length 710;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
RESULT 608
ID AAE17588 standard; protein; 710 AA.
DE Mycobacterium species M7B31F fusion protein.
PN W0200198460-A2.
PD 27-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 5; Length 710;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
RESULT 609
ID ADF69767 standard; protein; 710 AA.
DE Fusion protein #8 of M. tuberculosis antigen.
PN US2003147911-A1.
PD 07-AUG-2003.

PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 7; Length 710;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
RESULT 610
ID AAU74595 standard; protein; 723 AA.
DE Antigenic fusion protein DPV-M7I-MSL-M7CC2 (M7B1F).
PN US2002009459-A1.
PD 24-JAN-2002.
PA (REED/) REED S G.
PA (SKET/) SKETKY Y A.
PA (DILL/) DILLON D C.
PA (ALDE/) ALDERSON M.
PA (CAMP/) CAMPOS-NETO A.
Query Match 13.8%; Score 69.5; DB 5; Length 723;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
RESULT 611
ID AAY32064 standard; protein; 856 AA.
DE Mycobacterium tuberculosis antigen fusion protein M7B86F.
PN W09951748-A2.
PD 14-OCT-1999.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 2; Length 856;
Best Local Similarity 31.8%; Pred. No. 1.5e+02;
RESULT 612
ID ADF69763 standard; protein; 856 AA.
DE Fusion protein #6 of M. tuberculosis antigen.
PN US2003147911-A1.
PD 07-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 7; Length 856;
Best Local Similarity 31.8%; Pred. No. 1.5e+02;
RESULT 613
ID AAU74593 standard; protein; 859 AA.
DE Antigenic fusion protein Erid14-DPV-M7I-MSL-M7CC2 (M7B86F).
PN US2002009459-A1.
PD 24-JAN-2002.
PA (REED/) REED S G.
PA (SKET/) SKETKY Y A.
PA (DILL/) DILLON D C.
PA (ALDE/) ALDERSON M.
PA (CAMP/) CAMPOS-NETO A.
Query Match 13.8%; Score 69.5; DB 5; Length 859;
Best Local Similarity 31.8%; Pred. No. 1.5e+02;
RESULT 614
ID ADA26368 standard; protein; 1154 AA.
DE Mycobacterium M7B72F-M7CC#2 (fusion M7B114F) protein.
PN W02003070187-A2.
PD 28-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.8%; Score 69.5; DB 7; Length 1154;
Best Local Similarity 31.8%; Pred. No. 2.3e+02;
RESULT 615
ID ADU49404 standard; protein; 124 AA.
DE O11-associated gene related protein #904.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 13.7%; Score 69; DB 8; Length 124;
Best Local Similarity 31.8%; Pred. No. 14;
RESULT 616
ID ADR89163 standard; protein; 250 AA.
DE Amino acid sequence of a reductase.
PN EP1452588-A1.
PD 01-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 13.7%; Score 69; DB 8; Length 250;
Best Local Similarity 26.2%; Pred. No. 35;
RESULT 617
ID ADM19851 standard; protein; 291 AA.

DE Protein encoded by novel human channel/transporter gene #169.
 PN WO200154472-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 13.7%; Score 69; DB 4; Length 291;
 Best Local Similarity 32.1%; Pred. No. 42;

RESULT 618
 ID AD541606 standard; protein; 424 AA.
 DE Bacterial polypeptide #20036.

PN US200323675-A1.
 PD 18-DEC-2003.

PA (CAOY/) CNO Y.

PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

Query Match 13.7%; Score 69; DB 8; Length 424;
 Best Local Similarity 33.7%; Pred. No. 69;

RESULT 619

ID AAB43214 standard; protein; 431 AA.
 DE Human ORF2978 polypeptide sequence SEQ ID NO:5956.

PN WO200058473-A2.
 PD 05-OCT-2000.

PA (CURA-) CURAGEN CORP.

Query Match 13.7%; Score 69; DB 3; Length 431;
 Best Local Similarity 24.1%; Pred. No. 71;

RESULT 620

ID ABO79368 standard; protein; 468 AA.
 DE Pseudomonas aeruginosa polypeptide #11543.

PN US651795-B1.
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 13.7%; Score 69; DB 7; Length 468;
 Best Local Similarity 34.5%; Pred. No. 79;

RESULT 621

ID ABU19788 standard; protein; 470 AA.
 DE Protein encoded by Prokaryotic essential gene #5315.

PN WO200277183-A2.
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 13.7%; Score 69; DB 6; Length 470;
 Best Local Similarity 27.0%; Pred. No. 80;

RESULT 622

ID ADG33826 standard; protein; 479 AA.
 DE Actinomyces dual condensation/epimerisation NRS domain protein ID 85.

PN WO2003089641-A2.
 PD 30-OCT-2003.

PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match 13.7%; Score 69; DB 7; Length 479;
 Best Local Similarity 35.5%; Pred. No. 82;

RESULT 623

ID ABB63462 standard; protein; 569 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 17178.

PN WO200171042-A2.
 PD 27-SEP-2001.

PA (PEKE-) PE CORP NY.

Query Match 13.7%; Score 69; DB 4; Length 569;
 Best Local Similarity 25.2%; Pred. No. 1e+02;

RESULT 624

ID AAU61320 standard; protein; 628 AA.
 DE Propionibacterium acnes immunogenic protein #22216.

PN WO200181581-A2.
 PD 01-NOV-2001.

PA (CORI-) CORIXA CORP.

Query Match 13.7%; Score 69; DB 4; Length 628;
 Best Local Similarity 30.3%; Pred. No. 1.2e+02;

RESULT 625

ID ABM57839 standard; protein; 628 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #22515.

PN WO2003033515-A1.
 PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Best Local Similarity 30.3%; Pred. No. 1.2e+02;
 RESULT 626

ID ABO73535 standard; protein; 163 AA.
 DE Pseudomonas aeruginosa polypeptide #5710.

PN US651795-B1.
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 13.6%; Score 68.5; DB 7; Length 163;
 Best Local Similarity 34.3%; Pred. No. 22;

RESULT 627

ID ABP6027 standard; protein; 377 AA.
 DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:771.

PN EPI227152-A1.
 PD 31-JUL-2002.

PA (NEST-) SOC PROD NESTLE SA.

Query Match 13.6%; Score 68.5; DB 5; Length 377;
 Best Local Similarity 28.1%; Pred. No. 68;

RESULT 628

ID ABU3873 standard; protein; 404 AA.
 DE Protein encoded by Prokaryotic essential gene #19400.

PN WO200277183-A2.
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 13.6%; Score 68.5; DB 6; Length 404;
 Best Local Similarity 31.0%; Pred. No. 74;

RESULT 629

ID ABU33816 standard; protein; 434 AA.
 DE Protein encoded by Prokaryotic essential gene #19343.

PN WO200277183-A2.
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 13.6%; Score 68.5; DB 6; Length 434;
 Best Local Similarity 31.3%; Pred. No. 82;

RESULT 630

ID ABM65499 standard; protein; 436 AA.
 DE Propionibacterium acnes immunogenic polypeptide #30175.

PN WO2003033515-A1.
 PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Query Match 13.6%; Score 68.5; DB 6; Length 436;
 Best Local Similarity 34.8%; Pred. No. 82;

RESULT 631

ID ABU42281 standard; protein; 556 AA.
 DE Protein encoded by Prokaryotic essential gene #27808.

PN WO200277183-A2.
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 13.6%; Score 68.5; DB 6; Length 556;
 Best Local Similarity 26.9%; Pred. No. 1.1e+02;

RESULT 632

ID AAE32018 standard; protein; 1445 AA.
 DE Human blood cell surface antigen, CD109 #2.

PN WO200285942-A2.
 PD 31-OCT-2002.

PA (IVMC-) UNIV MCGILL.

Query Match 13.6%; Score 68.5; DB 6; Length 1445;
 Best Local Similarity 25.5%; Pred. No. 4e+02;

RESULT 633

ID AAU50922 standard; protein; 101 AA.
 DE Propionibacterium acnes immunogenic protein #11818.

PN WO200181581-A2.
 PD 01-NOV-2001.

PA (CORI-) CORIXA CORP.

Query Match 13.5%; Score 68; DB 4; Length 101;
 Best Local Similarity 35.3%; Pred. No. 14;

RESULT 634

ID ABM47441 standard; protein; 101 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #12117.

PN WO2003033515-A1.
 PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Query Match 13.5%; Score 68; DB 6; Length 101;
 Best Local Similarity 35.3%; Pred. No. 14;

RESULT 635
ID ABU25976 standard; protein; 126 AA.
DE Protein encoded by Prokaryotic essential gene #11503.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 13.5%; Score 68; DB 6; Length 126;
Best Local Similarity 33.3%; Pred. No. 18;
RESULT 636
ID AAU27346 standard; protein; 206 AA.
DE Novel bone marrow polypeptide #24.
PN WO200164840-A2.
PD 07-SEP-2001.
PA (HYSB-) HYSBQ INC.
Query Match 13.5%; Score 68; DB 4; Length 206;
Best Local Similarity 40.0%; Pred. No. 35;
RESULT 637
ID ABG29616 standard; protein; 339 AA.
DE Novel human diagnostic protein #29607.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 13.5%; Score 68; DB 4; Length 339;
Best Local Similarity 29.7%; Pred. No. 67;
RESULT 638
ID ABR42493 standard; protein; 377 AA.
DE Connermycin A1 biosynthetic decarboxylase.
PN WO2003014352-A2.
PD 20-FEB-2003.
PA (UYTU-) UNIV TUEBINGEN.
Query Match 13.5%; Score 68; DB 6; Length 377;
Best Local Similarity 28.7%; Pred. No. 77;
RESULT 639
ID ABU40451 standard; protein; 466 AA.
DE Protein encoded by Prokaryotic essential gene #25978.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 13.5%; Score 68; DB 6; Length 466;
Best Local Similarity 31.8%; Pred. No. 1e+02;
RESULT 640
ID ADP04395 standard; protein; 480 AA.
DE Bacterial polypeptide #508.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.5%; Score 68; DB 7; Length 480;
Best Local Similarity 31.8%; Pred. No. 1.1e+02;
RESULT 641
ID ABM68704 standard; protein; 590 AA.
DE Photorhabdus luminescens protein sequence #1801.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.5%; Score 68; DB 6; Length 590;
Best Local Similarity 29.3%; Pred. No. 1.4e+02;
RESULT 642
ID ABG28816 standard; protein; 896 AA.
DE Novel human diagnostic protein #28807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 13.5%; Score 68; DB 4; Length 896;
Best Local Similarity 29.7%; Pred. No. 2.4e+02;
RESULT 643
ID AAB36119 standard; protein; 9510 AA.
DE Streptomyces nodosus amphi gene encoded protein.
PN WO200297082-A2.
PD 05-DEC-2002.
PA (UYDU-) UNIV COLLEGE DUBLIN.
Query Match 13.5%; Score 68; DB 6; Length 9510;
Best Local Similarity 30.8%; Pred. No. 5.4e+03;

RESULT 644
ID APP65533 standard; protein; 227 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:277.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 13.4%; Score 67.5; DB 5; Length 227;
Best Local Similarity 29.6%; Pred. No. 45;
RESULT 645
ID AAU40714 standard; protein; 478 AA.
DE Propionibacterium acnes immunogenic protein #1610.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 67.5; DB 4; Length 478;
Best Local Similarity 25.0%; Pred. No. 1.2e+02;
RESULT 646
ID ABM37233 standard; protein; 478 AA.
DE Propionibacterium acnes membrane-related polypeptide #1909.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 67.5; DB 6; Length 478;
Best Local Similarity 25.0%; Pred. No. 1.2e+02;
RESULT 647
ID ABU36139 standard; protein; 1206 AA.
DE Protein encoded by Prokaryotic essential gene #21666.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 13.4%; Score 67.5; DB 6; Length 1206;
Best Local Similarity 29.4%; Pred. No. 4.1e+02;
RESULT 648
ID ABU26237 standard; protein; 1486 AA.
DE Aspergillus fumigatus essential gene protein #895.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 13.4%; Score 67.5; DB 6; Length 1486;
Best Local Similarity 30.6%; Pred. No. 5.3e+02;
RESULT 649
ID ADP56158 standard; protein; 2000 AA.
DE Human PRO protein sequence SEQ ID NO:2134.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 67.5; DB 8; Length 2000;
Best Local Similarity 29.2%; Pred. No. 7.9e+02;
RESULT 650
ID ABG79533 standard; protein; 2035 AA.
DE Human tumour suppressor protein #19.
PN WO200264775-A1.
PD 22-AUG-2002.
PA (BION-) BIONOMICS LTD.
Query Match 13.4%; Score 67.5; DB 5; Length 2035;
Best Local Similarity 29.2%; Pred. No. 8.1e+02;
RESULT 651
ID ADQ96094 standard; protein; 2035 AA.
DE T cell activation associated protein #136.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH PHARMA CORP.
Query Match 13.4%; Score 67.5; DB 8; Length 2035;
Best Local Similarity 29.4%; Pred. No. 8.1e+02;
RESULT 652
ID ADR66316 standard; protein; 2035 AA.
DE Human prostatic carcinoma derived protein SEQ ID 170 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.

PA (PILA/) PILARSKY C.
Query Match 13.4%; Score 67.5; DB 8; Length 2035;
Best Local Similarity 29.2%; Pred. No. 8.1e+02;
RESULT 653
ID AD66658 standard; protein, 2035 AA.
DE Human prostatic carcinoma derived protein SEQ ID 170 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 13.4%; Score 67.5; DB 8; Length 2035;
Best Local Similarity 29.2%; Pred. No. 8.1e+02;
RESULT 654
ID ADP95975 standard; protein, 2428 AA.
DE Arabidopsis thaliana root extension-induction protein #2.
PN JP2004187564-A.
PD 08-JUL-2004.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 13.4%; Score 67.5; DB 8; Length 2428;
Best Local Similarity 32.1%; Pred. No. 1e+03;
RESULT 655
ID ABB67747 standard; protein, 109 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30033.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 13.3%; Score 67; DB 4; Length 109;
Best Local Similarity 40.0%; Pred. No. 20;
RESULT 656
ID ADI36330 standard; peptide; 109 AA.
DE Drosophila CG13068 polypeptide, seq id 28.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND-) DANA FARBER CANCER INST INC.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 13.3%; Score 67; DB 7; Length 109;
Best Local Similarity 40.0%; Pred. No. 20;
RESULT 657
ID AAY52205 standard; protein, 351 AA.
DE Mycobacterium leprae yj5D protein.
PN WO9954470-A2.
PD 28-OCT-1999.
PA (GLAX-) GLAXO GROUP LTD.
Query Match 13.3%; Score 67; DB 3; Length 351;
Best Local Similarity 34.5%; Pred. No. 91;
RESULT 658
ID ABU35772 standard; protein, 351 AA.
DE Protein encoded by Prokaryotic essential gene #21299.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.3%; Score 67; DB 6; Length 351;
Best Local Similarity 34.5%; Pred. No. 91;
RESULT 659
ID ABO78075 standard; protein, 419 AA.
DE Pseudomonas aeruginosa polypeptide #10250.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.3%; Score 67; DB 7; Length 419;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 660
ID ADS28907 standard; protein, 423 AA.
DE Bacterial polypeptide #1940.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 67; DB 8; Length 423;
Best Local Similarity 25.0%; Pred. No. 1.2e+02;
RESULT 661
ID ADC50032 standard; protein, 469 AA.
DE Human macroprotein-51.59.
PN CN1382720-A.
PD 04-DEC-2002.
PA (BIOW-) BOWINDOM GENE DEV INC SHANGHAI.
Query Match 13.3%; Score 67; DB 7; Length 469;
Best Local Similarity 36.4%; Pred. No. 1.3e+02;
RESULT 662
ID ADG37784 standard; protein, 469 AA.
DE Actinomyces dual condensation/epimerisation NRPS domain protein ID 43.
PN WO2003089641-A2.
PD 30-OCT-2003.
PA (ECOP-) ECOPRIA BIOSCIENCES INC.
Query Match 13.3%; Score 67; DB 7; Length 469;
Best Local Similarity 28.3%; Pred. No. 1.3e+02;
RESULT 663
ID ADS21155 standard; protein, 624 AA.
DE Bacterial polypeptide #10188.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 67; DB 8; Length 624;
Best Local Similarity 35.8%; Pred. No. 1.9e+02;
RESULT 664
ID ADS27851 standard; protein, 724 AA.
DE Bacterial polypeptide #16884.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 67; DB 8; Length 724;
Best Local Similarity 30.4%; Pred. No. 2.4e+02;
RESULT 665
ID ABU40135 standard; protein, 854 AA.
DE Protein encoded by Prokaryotic essential gene #25662.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.3%; Score 67; DB 6; Length 854;
Best Local Similarity 28.6%; Pred. No. 2.9e+02;
RESULT 666
ID ABM85277 standard; protein, 1249 AA.
DE Human protein sequence hCP1635124.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.3%; Score 67; DB 7; Length 1249;
Best Local Similarity 36.4%; Pred. No. 4.8e+02;
RESULT 667
ID AAR14108 standard; protein, 180 AA.
DE Zea mays 15 kd seed storage protein.
PN WO9113993-A.
PD 19-SEP-1991.
PA (UPUC-) UPJOHN CO.
Query Match 13.2%; Score 66.5; DB 2; Length 180;
Best Local Similarity 38.6%; Pred. No. 43;
RESULT 668
ID ABU41499 standard; protein, 322 AA.
DE Protein encoded by Prokaryotic essential gene #27026.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

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Query Match      13.2%; Score 66.5; DB 6; Length 322;
Best Local Similarity 27.4%; Pred. No. 92;
RESULT 669
ID ABO67390 standard; protein; 323 AA.
DE Klebsiella pneumoniae polypeptide seqid 13907.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.2%; Score 66.5; DB 7; Length 323;
Best Local Similarity 30.9%; Pred. No. 93;
RESULT 670
ID ADB75312 standard; protein; 465 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match      13.2%; Score 66.5; DB 7; Length 465;
Best Local Similarity 28.9%; Pred. No. 1.5e+02;
RESULT 671
ID ABB93369 standard; protein; 491 AA.
DE Herbicidally active polypeptide SEQ ID NO 2580.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
Query Match      13.2%; Score 66.5; DB 5; Length 491;
Best Local Similarity 28.3%; Pred. No. 1.6e+02;
RESULT 672
ID ADN24365 standard; protein; 667 AA.
DE Bacterial polypeptide #7018.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      13.2%; Score 66.5; DB 8; Length 667;
Best Local Similarity 31.6%; Pred. No. 2.4e+02;
RESULT 673
ID ADF61855 standard; protein; 115 AA.
DE G3-2H6 protein which is derived from DNA antisense to human DDX9 DNA.
PN WO2003088910-A2.
PD 30-OCT-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match      13.1%; Score 66; DB 7; Length 115;
Best Local Similarity 32.8%; Pred. No. 27;
RESULT 674
ID ABO66080 standard; protein; 310 AA.
DE Klebsiella pneumoniae polypeptide seqid 12597.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.1%; Score 66; DB 7; Length 310;
Best Local Similarity 28.6%; Pred. No. 1e+02;
RESULT 675
ID ABU43577 standard; protein; 330 AA.
DE Protein encoded by Prokaryotic essential gene #35104.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      13.1%; Score 66; DB 6; Length 330;
Best Local Similarity 31.5%; Pred. No. 1.1e+02;
RESULT 676
ID ABM85476 standard; protein; 332 AA.
DE Mouse protein sequence mcp5983.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match      13.1%; Score 66; DB 7; Length 332;
Best Local Similarity 38.6%; Pred. No. 1.1e+02;
RESULT 677
ID ADR06365 standard; protein; 370 AA.
DE N meningitidis P1:22,14 PorA protein SeqID25.
PN WO2004065603-A2.
PD 05-AUG-2004.
PA (AMHP ) WYETH HOLDINGS CORP.
Query Match      13.1%; Score 66; DB 8; Length 370;
Best Local Similarity 28.7%; Pred. No. 1.3e+02;
RESULT 678
ID AAY42520 standard; protein; 390 AA.
DE Maize anthranilate phosphoribosyltransferase.
PN WO9949013-A2.
PD 30-SEP-1999.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match      13.1%; Score 66; DB 2; Length 390;
Best Local Similarity 23.5%; Pred. No. 1.4e+02;
RESULT 679
ID ABU20063 standard; protein; 440 AA.
DE Protein encoded by Prokaryotic essential gene #5590.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      13.1%; Score 66; DB 6; Length 440;
Best Local Similarity 27.5%; Pred. No. 1.6e+02;
RESULT 680
ID AAU62614 standard; protein; 543 AA.
DE Propionibacterium acnes immunogenic protein #23510.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match      13.1%; Score 66; DB 4; Length 543;
Best Local Similarity 29.1%; Pred. No. 2.1e+02;
RESULT 681
ID ABM59133 standard; protein; 543 AA.
DE Propionibacterium acnes membrane-related polypeptide #23809.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match      13.1%; Score 66; DB 6; Length 543;
Best Local Similarity 29.1%; Pred. No. 2.1e+02;
RESULT 682
ID ADS23240 standard; protein; 581 AA.
DE Bacterial polypeptide #12273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      13.1%; Score 66; DB 8; Length 581;
Best Local Similarity 27.9%; Pred. No. 2.3e+02;
RESULT 683
ID ABO82733 standard; protein; 587 AA.
DE Pseudomonas aeruginosa polypeptide #14908.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.1%; Score 66; DB 7; Length 587;
Best Local Similarity 30.6%; Pred. No. 2.3e+02;
RESULT 684
ID AAR32007 standard; protein; 638 AA.
DE Herbicide sensitive AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match      13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 685
ID AAR32008 standard; protein; 638 AA.
DE Herbicide sensitive AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match      13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
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RESULT 686
ID AAR32006 standard; protein; 638 AA.
DE Herbicide resistant AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
  13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
ID AAW54055 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
  13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 688
ID AAW54054 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
  13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 689
ID AAW54053 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
  13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 690
ID ABG71110 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) mutant #2.
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
  13.1%; Score 66; DB 5; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 691
ID ABG71108 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) .
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
  13.1%; Score 66; DB 5; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 692
ID ABG71109 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) mutant #1.
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
  13.1%; Score 66; DB 5; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 693
ID AAW18306 standard; protein; 1043 AA.
DE Photorhabdus luminescens insect toxin Tccc.
PN WO9717432-A1.
PD 15-MAY-1997.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
Query Match
  13.1%; Score 66; DB 2; Length 1043;
Best Local Similarity 26.4%; Pred. No. 4.9e+02;
RESULT 694
ID AAW56569 standard; protein; 1043 AA.
DE Toxin Tccc, encoded by the tccc gene from genomic region tcc.
PN WO9808932-A1.
PD 05-MAR-1998.
PA (DOMC ) DOWELANCO.
Query Match
  13.1%; Score 66; DB 2; Length 1043;
Best Local Similarity 26.4%; Pred. No. 4.9e+02;
RESULT 695
ID ADR21577 standard; protein; 1043 AA.
DE Photorhabdus Tccc1 toxin.
PN WO200406727-A2.
PD 12-AUG-2004.
PA (DOMC ) DOW AGROSCIENCES LLC.
Query Match
  13.1%; Score 66; DB 8; Length 1043;
Best Local Similarity 26.4%; Pred. No. 4.9e+02;
RESULT 696
ID ABU05722 standard; protein; 1400 AA.
DE M. tuberculosis and M. leprae marker protein #373.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTERUR.
Query Match
  13.1%; Score 66; DB 5; Length 1400;
Best Local Similarity 26.2%; Pred. No. 7.3e+02;
RESULT 697
ID ABB58564 standard; protein; 1664 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2484.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
  13.1%; Score 66; DB 4; Length 1664;
Best Local Similarity 34.2%; Pred. No. 9.1e+02;
RESULT 698
ID ADR09003 standard; protein; 119 AA.
DE Human protein useful for treating neurological disease Seq 2509.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
  13.0%; Score 65.5; DB 8; Length 119;
Best Local Similarity 28.2%; Pred. No. 32;
RESULT 699
ID AAU76435 standard; protein; 319 AA.
DE Novel desulphurising microbe associated protein #2.
PN JP2001309788-A.
PD 06-NOV-2001.
PA (SEKI-) ZH SEKIYU SANGYO KASSRIKA CENTER.
Query Match
  13.0%; Score 65.5; DB 5; Length 319;
Best Local Similarity 26.5%; Pred. No. 1.2e+02;
RESULT 700
ID AAU55341 standard; protein; 321 AA.
DE Enterococcus faecalis cellular proliferation protein #628.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
  13.0%; Score 65.5; DB 4; Length 321;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 701
ID ABU29413 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #14940.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
  13.0%; Score 65.5; DB 6; Length 321;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 702
ID ADH86584 standard; protein; 346 AA.
DE Enterococcus faecalis polypeptide #1064.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
Query Match
  13.0%; Score 65.5; DB 7; Length 346;
Best Local Similarity 25.2%; Pred. No. 1.3e+02;
RESULT 703
ID ABO64338 standard; protein; 407 AA.
DE Klebsiella pneumoniae polypeptide seqid 10855.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
  13.0%; Score 65.5; DB 7; Length 407;
Best Local Similarity 29.1%; Pred. No. 1.6e+02;
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RESULT 704
ID ABU0589 standard; protein; 491 AA.
DE M. tuberculosis and M. leprae marker protein #540.
PN W0200274903-A2.
PD 26-SEP-2002.
PA (INSP-) INSTR PASTEUR.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 5; Length 491;
RESULT 705
ID ADL22688 standard; protein; 529 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 137.
PN W02003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 7; Length 529;
RESULT 706
ID ADF05855 standard; protein; 645 AA.
DE Bacterial polypeptide #1968.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 7; Length 645;
RESULT 707
ID ADC97736 standard; protein; 803 AA.
DE Rhizobitoxine ttxc gene derived protein, SEQ ID No 9.
PN JP2003093069-A.
PD 02-APR-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 7; Length 803;
RESULT 708
ID ABU23297 standard; protein; 808 AA.
DE Protein encoded by Prokaryotic essential gene #8824.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 6; Length 808;
RESULT 709
ID ABU3614 standard; protein; 848 AA.
DE Protein encoded by Prokaryotic essential gene #21641.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 6; Length 848;
RESULT 710
ID ADS42058 standard; protein; 857 AA.
DE Bacterial polypeptide #20488.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 857;
RESULT 711
ID ADN26721 standard; protein; 857 AA.
DE Bacterial polypeptide #9374.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 857;
RESULT 712
ID ADM48067 standard; protein; 861 AA.
DE Polypeptide sequence #117 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 861;
RESULT 713
ID ADS28481 standard; protein; 861 AA.
DE Bacterial polypeptide #17514.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 861;
RESULT 714
ID ABG06406 standard; protein; 974 AA.
DE Novel human diagnostic protein #6397.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 4; Length 974;
RESULT 715
ID ABO59456 standard; protein; 1633 AA.
DE Human genome derived single exon protein #5690.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 1633;
RESULT 716
ID ADO97066 standard; protein; 2250 AA.
DE Human cancer associated sequence HP11-012, SEQ ID 42.
PN W02004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 2250;
RESULT 717
ID ABR58648 standard; protein; 2303 AA.
DE Human cancer related protein SEQ ID NO:305.
PN W02003025138-A2.
PD 27-MAR-2003.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 6; Length 2303;
RESULT 718
ID ADO08045 standard; protein; 2303 AA.
DE Human polypeptide #46.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 2303;
RESULT 719
ID AAB70968 standard; protein; 4924 AA.
DE S. spinosa protein fragment encoded by ORF21, SEQ ID 48.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (PARB-) BAYER AG.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 4; Length 4924;
RESULT 720
ID AAY39300 standard; protein; 4928 AA.
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DE Spnd a polyketide synthase.
PN WO9946387-A1.
PD 16-SEP-1999.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 13.0%; Score 65.5; DB 2; Length 4928;
Best Local Similarity 28.6%; Pred. No. 4.3e+03;
RESULT 721
ID AAG53754 standard; protein; 178 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66467.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 65; DB 3; Length 178;
Best Local Similarity 30.1%; Pred. No. 63;
RESULT 722
ID ABO65795 standard; protein; 180 AA.
DE Klebsiella pneumoniae polypeptide seqid 12312.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 65; DB 7; Length 180;
Best Local Similarity 26.3%; Pred. No. 63;
RESULT 723
ID ABU34031 standard; protein; 260 AA.
DE Protein encoded by Prokaryotic essential gene #19558.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 65; DB 6; Length 260;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 724
ID AAB79808 standard; protein; 267 AA.
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:350.
PN WO200100843-A2.
PD 04-JAN-2001.
PA (BADT) BASF AG.
Query Match 12.9%; Score 65; DB 4; Length 267;
Best Local Similarity 34.8%; Pred. No. 1.1e+02;
RESULT 725
ID AAG89997 standard; protein; 267 AA.
DE C glutamicum protein fragment SEQ ID NO: 3751.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.9%; Score 65; DB 4; Length 267;
Best Local Similarity 34.8%; Pred. No. 1.1e+02;
RESULT 726
ID ADC96055 standard; protein; 269 AA.
DE E. faecium protein sequence SEQ ID 5682.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 65; DB 7; Length 269;
Best Local Similarity 26.6%; Pred. No. 1.1e+02;
RESULT 727
ID AAB12308 standard; protein; 329 AA.
DE Human secreted protein encoded by gene 8 clone HCWEM59.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.9%; Score 65; DB 3; Length 329;
Best Local Similarity 31.9%; Pred. No. 1.4e+02;
RESULT 728
ID AAO72875 standard; protein; 350 AA.
DE Pseudomonas aeruginosa polypeptide #5050.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 65; DB 7; Length 350;
Best Local Similarity 29.5%; Pred. No. 1.5e+02;
RESULT 729
ID AAG4542 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55808.
PN EP1033405-A2.

PD 06-SEP-2000.
Query Match 12.9%; Score 65; DB 3; Length 452;
Best Local Similarity 30.1%; Pred. No. 2.1e+02;
RESULT 730
ID AAM52126 standard; protein; 457 AA.
DE Human alpha-2CAR variant protein.
PN WO200179561-A2.
PD 25-OCT-2001.
PA (LIGG/) LIGGETT S. B.
Query Match 12.9%; Score 65; DB 4; Length 457;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 731
ID AAK54834 standard; protein; 458 AA.
DE Human derived adrenalin alpha 2CII receptor.
PN JP6121686-A.
PD 06-MAY-1994.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 12.9%; Score 65; DB 2; Length 458;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 732
ID ADM37054 standard; protein; 458 AA.
DE Human alpha-2C adrenergic receptor variant protein SEQ ID NO:7.
PN WO2004023101-A2.
PD 18-MAR-2004.
PA (UYCI-) UNIV CINCINNATI.
Query Match 12.9%; Score 65; DB 8; Length 458;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 733
ID AAM52124 standard; protein; 461 AA.
DE Human alpha-2CAR protein.
PN WO200179561-A2.
PD 25-OCT-2001.
PA (LIGG/) LIGGETT S. B.
Query Match 12.9%; Score 65; DB 4; Length 461;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 734
ID ABB1781 standard; protein; 461 AA.
DE Human alpha 2c-adrenoceptor protein SEQ ID NO:44.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 12.9%; Score 65; DB 6; Length 461;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 735
ID ADU68565 standard; protein; 461 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID371.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 12.9%; Score 65; DB 8; Length 461;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 736
ID AD029175 standard; protein; 461 AA.
DE Human GPCR ADRA2C, SEQ ID NO:276.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 12.9%; Score 65; DB 8; Length 461;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 737
ID ADQ18949 standard; protein; 461 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1768.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.9%; Score 65; DB 8; Length 461;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 738
ID ADM37052 standard; protein; 462 AA.
DE Human alpha-2C adrenergic receptor protein SEQ ID NO:5.

PN WO2004023101-A2.
PD 18-MAR-2004.
PA (UYCI-) UNIV CINCINNATI.
Query Match 12.9%; Score 65; DB 8; Length 462;
Best Local Similarity 32.6%; Pred. No. 2.2e+02;
RESULT 739
ID ABG10418 standard; protein; 553 AA.
DE Novel human diagnostic protein #10409.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 65; DB 4; Length 553;
Best Local Similarity 30.2%; Pred. No. 2.8e+02;
RESULT 740
ID ABG08254 standard; protein; 622 AA.
DE Novel human diagnostic protein #8245.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 65; DB 4; Length 622;
Best Local Similarity 30.6%; Pred. No. 3.2e+02;
RESULT 741
ID AAR05588 standard; protein; 638 AA.
DE Acetylhydroxy acid synthetase (AHAS) from maize C1 genome.
PN EP360750-A.
PD 28-MAR-1990.
PA (CIBA) CIBA GEIGY AG.
Query Match 12.9%; Score 65; DB 2; Length 638;
Best Local Similarity 25.3%; Pred. No. 3.4e+02;
RESULT 742
ID AAG98345 standard; protein; 693 AA.
DE Escherichia coli protein sequence SEQ ID NO:393.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 65; DB 4; Length 693;
Best Local Similarity 30.2%; Pred. No. 3.7e+02;
RESULT 743
ID ABO71319 standard; protein; 703 AA.
DE Pseudomonas aeruginosa polypeptide #3494.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 65; DB 7; Length 703;
Best Local Similarity 28.1%; Pred. No. 3.8e+02;
RESULT 744
ID ABP43735 standard; protein; 725 AA.
DE DKFZP434E192 protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 65; DB 5; Length 725;
Best Local Similarity 30.6%; Pred. No. 4e+02;
RESULT 745
ID ABU22751 standard; protein; 757 AA.
DE Protein encoded by Prokaryotic essential gene #8278.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 65; DB 6; Length 757;
Best Local Similarity 31.9%; Pred. No. 4.2e+02;
RESULT 746
ID ABG79521 standard; protein; 832 AA.
DE Human tumour suppressor protein #7.
PN WO200264775-A1.
PD 22-AUG-2002.
PA (BION-) BIONOMICS LTD.
Query Match 12.9%; Score 65; DB 5; Length 832;
Best Local Similarity 30.6%; Pred. No. 4.8e+02;
RESULT 747
ID ABG08255 standard; protein; 852 AA.
DE Novel human diagnostic protein #8246.
PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 65; DB 4; Length 852;
Best Local Similarity 30.6%; Pred. No. 4.9e+02;
RESULT 748
ID AAU40390 standard; protein; 885 AA.
DE Propionibacterium acnes immunogenic protein #1286.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (COR-) CORIXA CORP.
Query Match 12.9%; Score 65; DB 4; Length 885;
Best Local Similarity 23.0%; Pred. No. 5.2e+02;
RESULT 749
ID ABM36909 standard; protein; 885 AA.
DE Propionibacterium acnes protease/proteinase-related polypeptide #1585.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (COR-) CORIXA CORP.
Query Match 12.9%; Score 65; DB 6; Length 885;
Best Local Similarity 23.0%; Pred. No. 5.2e+02;
RESULT 750
ID ABG97452 standard; protein; 1892 AA.
DE S. aerocolonigenes PKSE protein.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPRIA BIOSCIENCES INC.
Query Match 12.9%; Score 65; DB 5; Length 1892;
Best Local Similarity 28.4%; Pred. No. 1.4e+03;
RESULT 751
ID ADN20770 standard; protein; 2081 AA.
DE Bacterial polypeptide #3423.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 65; DB 8; Length 2081;
Best Local Similarity 23.5%; Pred. No. 1.6e+03;
RESULT 752
ID ADE55508 standard; protein; 2622 AA.
DE Rat Protein AACT8143, SEQ ID NO 1325.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.9%; Score 65; DB 7; Length 2622;
Best Local Similarity 27.7%; Pred. No. 2.2e+03;
RESULT 753
ID ABB64188 standard; protein; 2857 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19356.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.9%; Score 65; DB 4; Length 2857;
Best Local Similarity 32.7%; Pred. No. 2.4e+03;
RESULT 754
ID ABG99872 standard; protein; 4106 AA.
DE S. cinamomensis MonAV/polyketide synthase multi-enzyme MONS5.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
Query Match 12.9%; Score 65; DB 4; Length 4106;
Best Local Similarity 27.7%; Pred. No. 3.9e+03;
RESULT 755
ID ABG00972 standard; protein; 4274 AA.
DE Novel human diagnostic protein #963.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 65; DB 4; Length 4274;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;

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RESULT 756
ID ABG07375 standard; protein; 4386 AA.
DE Novel human diagnostic protein #7366.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 4; Length 4386;
RESULT 757
ID ABG21944 standard; protein; 4397 AA.
DE Novel human diagnostic protein #21935.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 4; Length 4397;
RESULT 758
ID ADG91698 standard; protein; 8147 AA.
DE Polypeptide synthase ORF10 protein, SEQ ID 21.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOP1A BIOSCIENCES INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 8147;
RESULT 759
ID ADP31311 standard; protein; 10944 AA.
DE Human secreted protein SEQ ID #2078.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 10944;
RESULT 760
ID ADP31310 standard; protein; 11328 AA.
DE Human secreted protein SEQ ID #2077.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 11328;
RESULT 761
ID ABB06921 standard; protein; 159 AA.
DE Micromonospora carbonacea evernimycin locus protein ORF 40.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOP1A BIOSCIENCES INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 159;
RESULT 762
ID AAG83022 standard; protein; 203 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:3138.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 203;
RESULT 763
ID AAP82484 standard; protein; 294 AA.
DE Tropoelactin.
PN JP63014694-A.
PD 21-JAN-1988.
PA (SHIS) SHISEIDO CO LTD.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 1; Length 294;
RESULT 764
ID ABO69335 standard; protein; 308 AA.
DE Pseudomonas aeruginosa polypeptide #1510.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 308;
RESULT 765
ID ABO79277 standard; protein; 310 AA.
DE Pseudomonas aeruginosa polypeptide #11452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 310;
RESULT 766
ID ABU43211 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #28738.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 6; Length 321;
RESULT 767
ID ABP39992 standard; protein; 326 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4837.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 5; Length 326;
RESULT 768
ID ADS07056 standard; protein; 326 AA.
DE Staphylococcus epidermidis polypeptide seqid 6351.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 326;
RESULT 769
ID ABO83285 standard; protein; 342 AA.
DE Pseudomonas aeruginosa polypeptide #15460.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 342;
RESULT 770
ID ADN22084 standard; protein; 416 AA.
DE Bacterial polypeptide #4737.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 416;
RESULT 771
ID ADN24843 standard; protein; 416 AA.
DE Bacterial polypeptide #7496.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 416;
RESULT 772
ID ABU47347 standard; protein; 433 AA.
DE Protein encoded by Prokaryotic essential gene #32874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 6; Length 433;
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Best Local Similarity 32.1%; Pred. No. 2.3e+02;
RESULT 773
ID ABU21899 standard; protein; 493 AA.
DE Protein encoded by Prokaryotic essential gene #7426.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.8%; Score 64.5; DB 6; Length 493;
Best Local Similarity 30.3%; Pred. No. 2.7e+02;
RESULT 774
ID ABG70144 standard; protein; 548 AA.
DE Human prey protein for Shigella ipac #8.
PN WO200257303-A2.
PD 25-JUL-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.8%; Score 64.5; DB 5; Length 548;
Best Local Similarity 24.3%; Pred. No. 3.1e+02;
RESULT 775
ID ADO80215 standard; protein; 594 AA.
DE Actinobacillus pleuropneumoniae Aprt exotoxin.
PN WO2004045639-A1.
PD 03-JUN-2004.
PA (HIPR-) LAB HIPRA SA.
Query Match 12.8%; Score 64.5; DB 8; Length 594;
Best Local Similarity 29.6%; Pred. No. 3.5e+02;
RESULT 776
ID ADS42744 standard; protein; 620 AA.
DE Bacterial polypeptide #21174.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.8%; Score 64.5; DB 8; Length 620;
Best Local Similarity 34.4%; Pred. No. 3.7e+02;
RESULT 777
ID ABU41121 standard; protein; 624 AA.
DE Protein encoded by Prokaryotic essential gene #26648.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.8%; Score 64.5; DB 6; Length 624;
Best Local Similarity 33.3%; Pred. No. 3.7e+02;
RESULT 778
ID ADP31265 standard; protein; 642 AA.
DE Human secreted protein SEQ ID #2032.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.8%; Score 64.5; DB 8; Length 642;
Best Local Similarity 40.0%; Pred. No. 3.8e+02;
RESULT 779
ID ABG70135 standard; protein; 698 AA.
DE Human prey protein for Shigella ipad #12.
PN WO200257303-A2.
PD 25-JUL-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.8%; Score 64.5; DB 5; Length 698;
Best Local Similarity 24.3%; Pred. No. 4.3e+02;
RESULT 780
ID ABM61192 standard; protein; 805 AA.
DE Propionibacterium acnes immunogenic polypeptide #29868.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.8%; Score 64.5; DB 6; Length 805;
Best Local Similarity 29.0%; Pred. No. 5.2e+02;
RESULT 781
ID ADN26513 standard; protein; 857 AA.
DE Bacterial polypeptide #9166.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.8%; Score 64.5; DB 8; Length 857;
Best Local Similarity 33.3%; Pred. No. 5.6e+02;
RESULT 782
ID AAU60702 standard; protein; 890 AA.
DE Propionibacterium acnes immunogenic protein #21598.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.8%; Score 64.5; DB 4; Length 890;
Best Local Similarity 29.0%; Pred. No. 5.9e+02;
RESULT 783
ID ABM57221 standard; protein; 890 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21897.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.8%; Score 64.5; DB 6; Length 890;
Best Local Similarity 29.0%; Pred. No. 5.9e+02;
RESULT 784
ID ABO82712 standard; protein; 906 AA.
DE Pseudomonas aeruginosa polypeptide #14887.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.8%; Score 64.5; DB 7; Length 906;
Best Local Similarity 30.0%; Pred. No. 6.1e+02;
RESULT 785
ID ADC00492 standard; protein; 952 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 537.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 12.8%; Score 64.5; DB 7; Length 952;
Best Local Similarity 29.9%; Pred. No. 6.5e+02;
RESULT 786
ID AAM22152 standard; protein; 1022 AA.
DE Apixia protein.
PN CA2170839-A.
PD 02-SEP-1996.
PA (UYGU-) UNIV GUELPH.
Query Match 12.8%; Score 64.5; DB 2; Length 1022;
Best Local Similarity 29.6%; Pred. No. 7.1e+02;
RESULT 787
ID AAY51406 standard; protein; 1022 AA.
DE A. pleuropneumoniae apxia protein.
PN US6019984-A.
PD 01-FEB-2000.
PA (UYGU-) UNIV GUELPH.
Query Match 12.8%; Score 64.5; DB 3; Length 1022;
Best Local Similarity 29.6%; Pred. No. 7.1e+02;
RESULT 788
ID AAR76991 standard; protein; 1023 AA.
DE Lhaa (low homology to appA) protein.
PN JP07138185-A.
PD 30-MAY-1995.
PA (NISK) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.
Query Match 12.8%; Score 64.5; DB 2; Length 1023;
Best Local Similarity 29.6%; Pred. No. 7.1e+02;
RESULT 789
ID ADC00339 standard; protein; 1026 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 384.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 12.8%; Score 64.5; DB 7; Length 1026;
Best Local Similarity 29.9%; Pred. No. 7.1e+02;
RESULT 790

ID ADN20624 standard; protein; 1026 AA.
DE Bacterial polypeptide #3277.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
ID (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 1026;
RESULT 791
ID ADC00043 standard; protein; 1080 AA.
DE Enterohemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 88.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 1080;
RESULT 792
ID ABO74881 standard; protein; 1413 AA.
DE Pseudomonas aeruginosa polypeptide #7056.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 1413;
RESULT 793
ID AAY92060 standard; protein; 1674 AA.
DE Murine APC-2 polypeptide.
PN WO20018913-A1.
PD 06-APR-2000.
PA (UYUT-) RIJKSUNIV UTRECHT.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 3; Length 1674;
RESULT 794
ID AAB50674 standard; protein; 2274 AA.
DE Mouse APC-2 protein sequence SEQ ID NO:65.
PN WO200073328-A2.
PD 07-DEC-2000.
PA (DEVG-) DEVGEN NV.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 2274;
RESULT 795
ID ADO08047 standard; protein; 2274 AA.
DE Mouse polypeptide #43.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 2274;
RESULT 796
ID ABB71657 standard; protein; 2328 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41763.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 2328;
RESULT 797
ID AAB41087 standard; protein; 2541 AA.
DE Human ORFX ORF851 polypeptide sequence SEQ ID NO:1702.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 3; Length 2541;
RESULT 798
ID ADD45522 standard; protein; 2541 AA.
DE Human Protein Q9Y490, SEQ ID NO 11186.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 2541;
RESULT 800
ID ADE58868 standard; protein; 2541 AA.
DE Human Protein Q9Y490, SEQ ID NO 4756.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 2541;
RESULT 801
ID ADE65318 standard; protein; 2541 AA.
DE Human talin 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 2541;
RESULT 802
ID ADE65318 standard; protein; 2541 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81738, SEQ:2683.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 2541;
RESULT 803
ID ADE65318 standard; protein; 2541 AA.
DE Human polypeptide sequence SEQ ID NO:1214.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.7%; Score 64; DB 7; Length 61;
RESULT 804
ID ADC67221 standard; protein; 277 AA.
DE Human GPCR protein SEQ ID NO:1674.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NMT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match
Best Local Similarity 12.7%; Score 64; DB 7; Length 277;
RESULT 805
ID ABB06890 standard; protein; 314 AA.
DE Micromonospora carbonacea evernimycin locus protein ORF 10.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 12.7%; Score 64; DB 4; Length 314;
RESULT 806
ID ABB99214 standard; protein; 314 AA.
DE Oribonomeycin biosynthetic polypeptide SEQ ID NO 15.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 12.7%; Score 64; DB 6; Length 314;

Best Local Similarity 29.9%; Pred. No. 1.7e+02;
RESULT 807
ID ABJ2589 standard; protein; 335 AA.
DE Aspergillus fumigatus essential gene protein #557.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.7%; Score 64; DB 6; Length 335;
Best Local Similarity 26.9%; Pred. No. 1.9e+02;
RESULT 808
ID ABO82719 standard; protein; 346 AA.
DE Pseudomonas aeruginosa polypeptide #14894.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 64; DB 7; Length 346;
Best Local Similarity 35.5%; Pred. No. 1.9e+02;
RESULT 809
ID ABJ26499 standard; protein; 392 AA.
DE Aspergillus fumigatus essential gene protein #1157.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.7%; Score 64; DB 6; Length 392;
Best Local Similarity 26.9%; Pred. No. 2.3e+02;
RESULT 810
ID ADN20982 standard; protein; 395 AA.
DE Bacterial polypeptide #3635.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.7%; Score 64; DB 8; Length 395;
Best Local Similarity 25.0%; Pred. No. 2.3e+02;
RESULT 811
ID ABO71901 standard; protein; 416 AA.
DE Pseudomonas aeruginosa polypeptide #4076.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 64; DB 7; Length 416;
Best Local Similarity 30.5%; Pred. No. 2.5e+02;
RESULT 812
ID ABU34364 standard; protein; 445 AA.
DE Protein encoded by Prokaryotic essential gene #19891.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.7%; Score 64; DB 6; Length 445;
Best Local Similarity 29.7%; Pred. No. 2.7e+02;
RESULT 813
ID AAY75759 standard; protein; 464 AA.
DE Neisseria meningitidis ORF 989 protein sequence SEQ ID NO:2990.
PN W09557280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 12.7%; Score 64; DB 3; Length 464;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 814
ID ABU37723 standard; protein; 464 AA.
DE Protein encoded by Prokaryotic essential gene #23250.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.7%; Score 64; DB 6; Length 464;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 815
ID AAB01258 standard; protein; 466 AA.
DE Neisseria meningitidis BASB044 protein #1.

PN W0200034482-A2.
PD 15-JUN-2000.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 12.7%; Score 64; DB 3; Length 466;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 816
ID ABG19694 standard; protein; 605 AA.
DE Novel human diagnostic protein #19685.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 64; DB 4; Length 605;
Best Local Similarity 37.3%; Pred. No. 4.1e+02;
RESULT 817
ID ADS27968 standard; protein; 693 AA.
DE Bacterial polypeptide #17001.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.7%; Score 64; DB 8; Length 693;
Best Local Similarity 25.6%; Pred. No. 4.8e+02;
RESULT 818
ID ABO79385 standard; protein; 836 AA.
DE Pseudomonas aeruginosa polypeptide #10560.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 64; DB 7; Length 836;
Best Local Similarity 22.4%; Pred. No. 6.2e+02;
RESULT 819
ID ABO79850 standard; protein; 996 AA.
DE Pseudomonas aeruginosa polypeptide #12025.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 64; DB 7; Length 996;
Best Local Similarity 30.9%; Pred. No. 7.8e+02;
RESULT 820
ID AAM69055 standard; protein; 1044 AA.
DE Photorhabdus luminescens protein sequence #2152.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS-) CNRS CENT NAT RECH SCI.
Query Match 12.7%; Score 64; DB 6; Length 1044;
Best Local Similarity 26.4%; Pred. No. 8.3e+02;
RESULT 821
ID AAB07563 standard; protein; 1218 AA.
DE Protein encoded by the bleomycin (BLM) gene cluster ORF30.
PN W0200040704-A1.
PD 13-JUL-2000.
PA (REGC-) UNIV CALIFORNIA.
Query Match 12.7%; Score 64; DB 3; Length 1218;
Best Local Similarity 48.0%; Pred. No. 1e+03;
RESULT 822
ID AAM70381 standard; protein; 1481 AA.
DE Photorhabdus luminescens protein sequence #3478.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS-) CNRS CENT NAT RECH SCI.
Query Match 12.7%; Score 64; DB 6; Length 1481;
Best Local Similarity 26.6%; Pred. No. 1.3e+02;
RESULT 823
ID ABG06301 standard; protein; 2017 AA.
DE Novel human diagnostic protein #6292.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

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Query Match                                12.7%; Score 64; DB 4; Length 2017;
Best Local Similarity 27.0%; Pred. No. 2e+03;
RESULT 824
ID ADS27816 standard; protein; 2479 AA.
DE Bacterial polypeptide #16849.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match                                12.7%; Score 64; DB 8; Length 2479;
Best Local Similarity 27.6%; Pred. No. 2.6e+03;
RESULT 825
ID AD139289 standard; protein; 6842 AA.
DE S. hygroscopicus geldanamycin gene cluster-encoded protein, SEQ ID:131.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Query Match                                12.7%; Score 64; DB 8; Length 6842;
Best Local Similarity 25.2%; Pred. No. 9.9e+03;
RESULT 826
ID AAG89188 standard; protein; 105 AA.
DE Human secreted protein, SEQ ID NO: 308.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST-) GENSET.
Query Match                                12.6%; Score 63.5; DB 4; Length 105;
Best Local Similarity 26.5%; Pred. No. 46;
RESULT 827
ID AAE20199 standard; protein; 106 AA.
DE Human mature haematopoietic growth factor-like protein.
PN WO200214491-A2.
PD 21-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match                                12.6%; Score 63.5; DB 5; Length 106;
Best Local Similarity 26.5%; Pred. No. 47;
RESULT 828
ID ABG66722 standard; protein; 115 AA.
DE Human novel polypeptide #57.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match                                12.6%; Score 63.5; DB 5; Length 115;
Best Local Similarity 26.5%; Pred. No. 52;
RESULT 829
ID AAO67973 standard; protein; 128 AA.
DE Propionibacterium acnes immunogenic protein #28869.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match                                12.6%; Score 63.5; DB 4; Length 128;
Best Local Similarity 28.7%; Pred. No. 60;
RESULT 830
ID ABW64492 standard; protein; 128 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #29168.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match                                12.6%; Score 63.5; DB 6; Length 128;
Best Local Similarity 28.7%; Pred. No. 60;
RESULT 831
ID AAE20198 standard; protein; 130 AA.
DE Human haematopoietic growth factor-like protein.
PN WO200214491-A2.
PD 21-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match                                12.6%; Score 63.5; DB 5; Length 130;
Best Local Similarity 26.5%; Pred. No. 61;
RESULT 832
ID ABU36045 standard; protein; 130 AA.
DE Protein encoded by Prokaryotic essential gene #21572.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match                                12.6%; Score 63.5; DB 6; Length 130;
Best Local Similarity 27.1%; Pred. No. 61;
RESULT 833
ID ADS44437 standard; protein; 175 AA.
DE Bacterial polypeptide #22867.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match                                12.6%; Score 63.5; DB 8; Length 175;
Best Local Similarity 32.1%; Pred. No. 90;
RESULT 834
ID AAB79884 standard; protein; 225 AA.
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:502.
PN WO200100843-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match                                12.6%; Score 63.5; DB 4; Length 225;
Best Local Similarity 30.4%; Pred. No. 1.3e+02;
RESULT 835
ID AAB79697 standard; protein; 225 AA.
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:128.
PN WO200100843-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match                                12.6%; Score 63.5; DB 4; Length 225;
Best Local Similarity 30.4%; Pred. No. 1.3e+02;
RESULT 836
ID ADL65943 standard; protein; 262 AA.
DE C. glutamicum RXA-associated protein #150.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI) BASF AG.
Query Match                                12.6%; Score 63.5; DB 7; Length 262;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 837
ID AAG91330 standard; protein; 263 AA.
DE C glutamicum protein fragment SEQ ID NO: 5084.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match                                12.6%; Score 63.5; DB 4; Length 263;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 838
ID ADN20914 standard; protein; 284 AA.
DE Bacterial polypeptide #3567.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match                                12.6%; Score 63.5; DB 8; Length 284;
Best Local Similarity 30.1%; Pred. No. 1.7e+02;
RESULT 839
ID ABU23091 standard; protein; 303 AA.
DE Protein encoded by Prokaryotic essential gene #6618.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match                                12.6%; Score 63.5; DB 6; Length 303;
Best Local Similarity 30.9%; Pred. No. 1.9e+02;
RESULT 840
ID AAB86984 standard; protein; 367 AA.
DE C. glutamicum ATCC 13032 dapC variant protein.
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PN EPI136559-A2.
PD 26-SEP-2001.
PA (DEGS) DEGUSSA-HUELS AG.
Query Match 12.6%; Score 63.5; DB 4; Length 367;
Best Local Similarity 30.4%; Pred. No. 2.4e+02;
RESULT 841
ID AAB86983 standard; protein; 367 AA.
DE C. glutamicum ATCC 13032 dapc protein.
PN EPI136559-A2.
PD 26-SEP-2001.
PA (DEGS) DEGUSSA-HUELS AG.
Query Match 12.6%; Score 63.5; DB 4; Length 367;
Best Local Similarity 30.4%; Pred. No. 2.4e+02;
RESULT 842
ID AAG90972 standard; protein; 367 AA.
DE C glutamicum protein fragment SEQ ID NO: 4726.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.6%; Score 63.5; DB 4; Length 367;
Best Local Similarity 30.4%; Pred. No. 2.4e+02;
RESULT 843
ID ADD13565 standard; protein; 367 AA.
DE C. glutamicum metabolic pathway protein RXA03003.
PN W02003040681-A2.
PD 15-MAY-2003.
PA (BADI) BASF AG.
Query Match 12.6%; Score 63.5; DB 7; Length 367;
Best Local Similarity 30.4%; Pred. No. 2.4e+02;
RESULT 844
ID AAU16363 standard; protein; 375 AA.
DE Human novel secreted protein, Seq ID 1316.
PN W0200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 63.5; DB 4; Length 375;
Best Local Similarity 35.8%; Pred. No. 2.5e+02;
RESULT 845
ID ABUS5432 standard; protein; 375 AA.
DE Human novel polypeptide #519.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.6%; Score 63.5; DB 6; Length 375;
Best Local Similarity 35.8%; Pred. No. 2.5e+02;
RESULT 846
ID AAU15910 standard; protein; 378 AA.
DE Human novel secreted protein, Seq ID 863.
PN W0200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 63.5; DB 4; Length 378;
Best Local Similarity 35.8%; Pred. No. 2.5e+02;
RESULT 847
ID ABUS4979 standard; protein; 378 AA.
DE Human novel polypeptide #66.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.6%; Score 63.5; DB 6; Length 378;
Best Local Similarity 35.8%; Pred. No. 2.5e+02;
RESULT 848
ID AAM43037 standard; protein; 394 AA.
DE Alcaligenes eutrophus beta-ketochiolase (Bktb).
PN W09800557-A2.
PD 08-JAN-1998.
PA (MONS) MONSANTO CO.
Query Match 12.6%; Score 63.5; DB 2; Length 394;
Best Local Similarity 30.3%; Pred. No. 2.6e+02;

RESULT 849
ID AAY29664 standard; protein; 394 AA.
DE A. eutrophus beta-ketochiolase protein.
PN US5942660-A.
PD 24-AUG-1999.
PA (MONS) MONSANTO CO.
Query Match 12.6%; Score 63.5; DB 2; Length 394;
Best Local Similarity 30.3%; Pred. No. 2.6e+02;
RESULT 850
ID AAB10567 standard; protein; 394 AA.
DE A. eutrophus bktb protein.
PN US6091002-A.
PD 18-JUL-2000.
PA (MONS) MONSANTO CO.
Query Match 12.6%; Score 63.5; DB 3; Length 394;
Best Local Similarity 30.3%; Pred. No. 2.6e+02;
RESULT 851
ID AAE05083 standard; protein; 394 AA.
DE Alcaligenes eutrophus Bktb beta-ketochiolase.
PN US6228623-B1.
PD 08-MAY-2001.
PA (MONS) MONSANTO CO.
Query Match 12.6%; Score 63.5; DB 4; Length 394;
Best Local Similarity 30.3%; Pred. No. 2.6e+02;
RESULT 852
ID ADN17447 standard; protein; 398 AA.
DE Bacterial polypeptide #100.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 63.5; DB 8; Length 398;
Best Local Similarity 30.0%; Pred. No. 2.7e+02;
RESULT 853
ID ABU35789 standard; protein; 407 AA.
DE Protein encoded by Prokaryotic essential gene #21316.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.6%; Score 63.5; DB 6; Length 407;
Best Local Similarity 35.4%; Pred. No. 2.7e+02;
RESULT 854
ID ABU39863 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #25390.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.6%; Score 63.5; DB 6; Length 458;
Best Local Similarity 27.7%; Pred. No. 3.2e+02;
RESULT 855
ID ABO80983 standard; protein; 467 AA.
DE Pseudomonas aeruginosa polypeptide #13158.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 63.5; DB 7; Length 467;
Best Local Similarity 32.1%; Pred. No. 3.3e+02;
RESULT 856
ID ABB06143 standard; protein; 475 AA.
DE Human NS protein sequence SEQ ID NO:235.
PN W0200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 12.6%; Score 63.5; DB 5; Length 475;
Best Local Similarity 23.6%; Pred. No. 3.4e+02;
RESULT 857
ID ABB92709 standard; protein; 519 AA.
DE Herbicidally active polypeptide SEQ ID NO 1920.
PN W0200210210-A2.
PD 07-FEB-2002.

PA (FARB) BAYER AG.
Query Match 12.6%; Score 63.5; DB 5; Length 519;
Best Local Similarity 31.6%; Pred. No. 3.8e+02;
RESULT 858
ID AABU19783 standard; protein; 529 AA.
DE Protein encoded by Prokaryotic essential gene #5310.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.6%; Score 63.5; DB 6; Length 529;
Best Local Similarity 30.9%; Pred. No. 3.9e+02;
RESULT 859
ID AAB79045 standard; protein; 537 AA.
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:46.
PN WO200100842-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 12.6%; Score 63.5; DB 4; Length 537;
Best Local Similarity 36.1%; Pred. No. 3.9e+02;
RESULT 860
ID ABO68319 standard; protein; 545 AA.
DE Pseudomonas aeruginosa polypeptide #494.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 63.5; DB 7; Length 545;
Best Local Similarity 30.1%; Pred. No. 4e+02;
RESULT 861
ID ABO68791 standard; protein; 594 AA.
DE Novel human diagnostic protein #8782.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 63.5; DB 4; Length 594;
Best Local Similarity 29.7%; Pred. No. 4.5e+02;
RESULT 862
ID ABU25746 standard; protein; 630 AA.
DE Protein encoded by Prokaryotic essential gene #11273.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.6%; Score 63.5; DB 6; Length 630;
Best Local Similarity 27.6%; Pred. No. 4.9e+02;
RESULT 863
ID AAW23036 standard; protein; 631 AA.
DE Human cytomegalovirus combined antigen.
PN WO9731117-A2.
PD 28-AUG-1997.
PA (UYMA-) UNIV MAASTRICHT.
Query Match 12.6%; Score 63.5; DB 2; Length 631;
Best Local Similarity 29.9%; Pred. No. 4.9e+02;
RESULT 864
ID AAB79044 standard; protein; 642 AA.
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:44.
PN WO200100842-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 12.6%; Score 63.5; DB 4; Length 642;
Best Local Similarity 36.1%; Pred. No. 5e+02;
RESULT 865
ID AAG89921 standard; protein; 689 AA.
DE C glutamicum protein fragment SEQ ID NO: 3675.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.6%; Score 63.5; DB 4; Length 689;
Best Local Similarity 36.1%; Pred. No. 5.5e+02;
RESULT 866
ID ABB64835 standard; protein; 692 AA.
DE Drosophila melanogaster polypeptide SHQ ID NO 21297.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 12.6%; Score 63.5; DB 4; Length 692;
Best Local Similarity 27.3%; Pred. No. 5.5e+02;
RESULT 867
ID ABO74992 standard; protein; 728 AA.
DE Pseudomonas aeruginosa polypeptide #7167.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 63.5; DB 7; Length 728;
Best Local Similarity 30.4%; Pred. No. 5.9e+02;
RESULT 868
ID ADP31648 standard; protein; 889 AA.
DE Human secreted protein SEQ ID #2415.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.6%; Score 63.5; DB 8; Length 889;
Best Local Similarity 24.0%; Pred. No. 7.7e+02;
RESULT 869
ID ABO83590 standard; protein; 937 AA.
DE Pseudomonas aeruginosa polypeptide #15765.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 63.5; DB 7; Length 937;
Best Local Similarity 27.6%; Pred. No. 8.2e+02;
RESULT 870
ID ADC00868 standard; protein; 1026 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SHQ ID NO: 913.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 12.6%; Score 63.5; DB 7; Length 1026;
Best Local Similarity 29.9%; Pred. No. 9.2e+02;
RESULT 871
ID ADJ92012 standard; protein; 1046 AA.
DE Human herpesvirus 5 UL32 protein.
PN WO200305332-A2.
PD 03-JUL-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 12.6%; Score 63.5; DB 7; Length 1046;
Best Local Similarity 29.9%; Pred. No. 9.5e+02;
RESULT 872
ID AAR20637 standard; protein; 1048 AA.
DE Human cytomegalovirus antigen pp150.
PN WO9200323-A.
PD 09-JAN-1992.
PA (WELL) WELLCOME FOUND LTD.
Query Match 12.6%; Score 63.5; DB 2; Length 1048;
Best Local Similarity 29.9%; Pred. No. 9.5e+02;
RESULT 873
ID AAW27277 standard; protein; 1048 AA.
DE Human cytomegalovirus tegument protein pp150.
PN WO9740165-A1.
PD 30-OCT-1997.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 12.6%; Score 63.5; DB 2; Length 1048;
Best Local Similarity 29.9%; Pred. No. 9.5e+02;
RESULT 874
ID ADR70657 standard; protein; 1048 AA.
DE Human cytomegalovirus phosphoprotein pp150 SHQ ID NO:16.
PN WO2004076645-A2.
PD 10-SEP-2004.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 12.6%; Score 63.5; DB 8; Length 1048;
Best Local Similarity 29.9%; Pred. No. 9.5e+02;
RESULT 875
ID ABB66662 standard; protein; 1064 AA.
DE Drosophila melanogaster polypeptide SHQ ID NO 26778.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.6%; Score 63.5; DB 4; Length 1064;

Best Local Similarity 33.0%; Pred. No. 9.7e+02;
RESULT 876
ID ADC87585 standard; protein; 1232 AA.
DE Human GPCR protein SEQ ID NO:2038.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 12.6%; Score 63.5; DB 7; Length 1232;
Best Local Similarity 28.3%; Pred. No. 1.2e+03;
RESULT 877
ID AAB07564 standard; protein; 2675 AA.
DE Protein encoded by the bleomycin (BLM) gene cluster ORF30.
PN WO200040704-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 12.6%; Score 63.5; DB 3; Length 2675;
Best Local Similarity 29.1%; Pred. No. 3.3e+03;
RESULT 878
ID ABG25572 standard; protein; 148 AA.
DE Novel human diagnostic protein #25563.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 63; DB 4; Length 148;
Best Local Similarity 33.3%; Pred. No. 82;
RESULT 879
ID ABG27610 standard; protein; 191 AA.
DE Novel human diagnostic protein #27601.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 63; DB 4; Length 191;
Best Local Similarity 27.3%; Pred. No. 1.2e+02;
RESULT 880
ID ADF06072 standard; protein; 231 AA.
DE Bacterial polypeptide #2185.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 63; DB 7; Length 231;
Best Local Similarity 27.2%; Pred. No. 1.5e+02;
RESULT 881
ID ABJ19731 standard; protein; 234 AA.
DE Human secreted protein amino acid sequence - SEQ ID NO 199.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 63; DB 6; Length 234;
Best Local Similarity 27.8%; Pred. No. 1.5e+02;
RESULT 882
ID ABP99802 standard; protein; 234 AA.
DE Human secreted protein SEQ ID NO 746.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 63; DB 6; Length 234;
Best Local Similarity 27.8%; Pred. No. 1.5e+02;
RESULT 883
ID ADC20538 standard; protein; 234 AA.
DE Human secreted protein - amino acid sequence #219.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 63; DB 7; Length 234;
Best Local Similarity 27.8%; Pred. No. 1.5e+02;
RESULT 884
ID AAB51653 standard; protein; 235 AA.
DE Human secreted protein sequence encoded by gene 34 SEQ ID NO:93.
PN WO200061620-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.

Query Match 12.5%; Score 63; DB 3; Length 235;
Best Local Similarity 27.8%; Pred. No. 1.5e+02;
RESULT 885
ID ADS14819 standard; protein; 239 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 374.
PN WO2004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 12.5%; Score 63; DB 8; Length 239;
Best Local Similarity 28.6%; Pred. No. 1.5e+02;
RESULT 886
ID ADN22097 standard; protein; 260 AA.
DE Bacterial polypeptide #4750.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOT/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 63; DB 8; Length 260;
Best Local Similarity 30.1%; Pred. No. 1.7e+02;
RESULT 887
ID ADN24856 standard; protein; 260 AA.
DE Bacterial polypeptide #7509.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOT/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 63; DB 8; Length 260;
Best Local Similarity 30.1%; Pred. No. 1.7e+02;
RESULT 888
ID ABB55068 standard; protein; 307 AA.
DE Lactococcus lactis protein petd.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 12.5%; Score 63; DB 5; Length 307;
Best Local Similarity 28.6%; Pred. No. 2.2e+02;
RESULT 889
ID ABG07376 standard; protein; 314 AA.
DE Novel human diagnostic protein #7367.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 63; DB 4; Length 314;
Best Local Similarity 26.2%; Pred. No. 2.2e+02;
RESULT 890
ID ABG18917 standard; protein; 316 AA.
DE Novel human diagnostic protein #18908.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 63; DB 4; Length 316;
Best Local Similarity 39.5%; Pred. No. 2.2e+02;
RESULT 891
ID ABU31572 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #17099.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 321;
Best Local Similarity 27.0%; Pred. No. 2.3e+02;
RESULT 892
ID ADC96915 standard; protein; 325 AA.
DE E faecium protein sequence encoded by gene 34 SEQ ID 6542.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 63; DB 7; Length 325;

Best Local Similarity 25.3%; Pred. No. 2.3e+02;
RESULT 893
ID ABO67512 standard; protein; 329 AA.
DE Klebsiella pneumoniae polypeptide segid 14029.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 63; DB 7; Length 329;
Best Local Similarity 27.0%; Pred. No. 2.4e+02;
RESULT 894
ID ABO67956 standard; protein; 360 AA.
DE Pseudomonas aeruginosa polypeptide #131.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 63; DB 7; Length 360;
Best Local Similarity 28.6%; Pred. No. 2.7e+02;
RESULT 895
ID ABO28808 standard; protein; 366 AA.
DE Novel human diagnostic protein #28799.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 63; DB 4; Length 366;
Best Local Similarity 29.9%; Pred. No. 2.7e+02;
RESULT 896
ID ABO22269 standard; protein; 373 AA.
DE Protein encoded by prokaryotic essential gene #7796.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 373;
Best Local Similarity 29.9%; Pred. No. 2.8e+02;
RESULT 897
ID ABO33669 standard; protein; 410 AA.
DE Staphylococcus aureus cellular proliferation protein #145.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 4; Length 410;
Best Local Similarity 29.3%; Pred. No. 3.1e+02;
RESULT 898
ID ABO82741 standard; protein; 410 AA.
DE Pseudomonas aeruginosa polypeptide #14916.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 63; DB 7; Length 410;
Best Local Similarity 26.7%; Pred. No. 3.1e+02;
RESULT 899
ID ADF14023 standard; protein; 413 AA.
DE Human endometrial-specific protein - SRQ ID 654.
PN WO2003059927-A1.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 12.5%; Score 63; DB 7; Length 413;
Best Local Similarity 27.8%; Pred. No. 3.2e+02;
RESULT 900
ID ADF37217 standard; protein; 414 AA.
DE Staphylococcus aureus cellular proliferation protein #1387.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 4; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 901
ID ADF36936 standard; protein; 414 AA.
DE Staphylococcus aureus cellular proliferation protein #1106.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 4; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;

RESULT 902
ID AAE02198 standard; protein; 414 AA.
DE Staphylococcus aureus beta-ketoacyl-ACP synthase II (FabF).
PN WO200130988-A1.
PD 03-MAY-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.5%; Score 63; DB 4; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 903
ID AAB62056 standard; protein; 414 AA.
DE S. aureus fadF polypeptide.
PN WO200116173-A1.
PD 08-MAR-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.5%; Score 63; DB 4; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 904
ID ABE16217 standard; protein; 414 AA.
DE Protein encoded by prokaryotic essential gene #1744.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 905
ID ABW73213 standard; protein; 414 AA.
DE Staphylococcus aureus protein #2453.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 12.5%; Score 63; DB 6; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 906
ID ADJ49574 standard; protein; 414 AA.
DE Oil-associated gene related protein #1074.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C. C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDENUX J. R.
PA (ROGE/) ROGERS J. A.
Query Match 12.5%; Score 63; DB 8; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 907
ID ADJ49181 standard; protein; 414 AA.
DE Oil-associated gene related protein #681.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C. C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDENUX J. R.
PA (ROGE/) ROGERS J. A.
Query Match 12.5%; Score 63; DB 8; Length 414;
Best Local Similarity 29.3%; Pred. No. 3.2e+02;
RESULT 908
ID ADS21831 standard; protein; 428 AA.
DE Bacterial polypeptide #10864.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G. J.
PA (SLAT/) SLATER S. C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B. S.
Query Match 12.5%; Score 63; DB 8; Length 428;
Best Local Similarity 26.6%; Pred. No. 3.3e+02;
RESULT 909
ID AAB66451 standard; protein; 434 AA.
DE Protein encoded by Mycobacterium tuberculosis Rv3018c gene.

PN WO200102555-A1.
PD 11-JAN-2001.
PA (INST) INST PASTEUR.
Query Match 12.5%; Score 63; DB 4; Length 434;
Best Local Similarity 29.7%; Pred. No. 3.4e+02;
RESULT 910
ID ABU6905 standard; protein; 434 AA.
DE Protein encoded by Prokaryotic essential gene #22432.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 434;
Best Local Similarity 29.7%; Pred. No. 3.4e+02;
RESULT 911
ID ABU45582 standard; protein; 454 AA.
DE Protein encoded by Prokaryotic essential gene #31109.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 454;
Best Local Similarity 23.1%; Pred. No. 3.6e+02;
RESULT 912
ID ABU3234 standard; protein; 494 AA.
DE Protein encoded by Prokaryotic essential gene #17761.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 494;
Best Local Similarity 29.4%; Pred. No. 4e+02;
RESULT 913
ID ABU19717 standard; protein; 513 AA.
DE Protein encoded by Prokaryotic essential gene #5244.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 513;
Best Local Similarity 29.9%; Pred. No. 4.2e+02;
RESULT 914
ID ADP9909 standard; protein; 517 AA.
DE C. albicans specific gene, CAYGR256W, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 8; Length 517;
Best Local Similarity 31.0%; Pred. No. 4.3e+02;
RESULT 915
ID ABU45027 standard; protein; 535 AA.
DE Protein encoded by Prokaryotic essential gene #30554.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 63; DB 6; Length 535;
Best Local Similarity 28.1%; Pred. No. 4.5e+02;
RESULT 916
ID ADS21023 standard; protein; 556 AA.
DE Bacterial polypeptide #10056.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 63; DB 8; Length 556;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
RESULT 917
ID AAB85851 standard; protein; 900 AA.
DE Human PMS2 protein.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 12.5%; Score 63; DB 4; Length 900;

Best Local Similarity 26.3%; Pred. No. 8.9e+02;
RESULT 918
ID AAR7909 standard; protein; 931 AA.
DE Human DNA repair protein hMLH2.
PN WO9520678-A1.
PD 03-AUG-1995.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 63; DB 2; Length 931;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 919
ID AAB85852 standard; protein; 932 AA.
DE Human PMS1 protein.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 12.5%; Score 63; DB 4; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 920
ID AAG63953 standard; protein; 932 AA.
DE Amino acid sequence of human mismatch repair protein PMS2.
PN WO200162945-A1.
PD 30-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
Query Match 12.5%; Score 63; DB 4; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 921
ID AAG63954 standard; protein; 932 AA.
DE Amino acid sequence of human mismatch repair protein PMS1.
PN WO200162945-A1.
PD 30-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
Query Match 12.5%; Score 63; DB 4; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 922
ID AAU98776 standard; protein; 932 AA.
DE Human post meiotic segregation increased, PMS1, protein.
PN WO200238750-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 5; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 923
ID AAE24357 standard; protein; 932 AA.
DE Human mismatch repair protein, PMS1.
PN WO200237967-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 5; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 924
ID AAO18553 standard; protein; 932 AA.
DE Human mismatch repair protein PMS1.
PN WO200254856-A1.
PD 18-JUL-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 5; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 925
ID AAE28277 standard; protein; 932 AA.
DE Human MLH2 protein.
PN US6416984-B1.
PD 09-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match	12.5%;	Score 63;	DB 5;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 926				
ID AAE24684 standard; protein; 932 AA.				
DE Human PMS1 protein.				
PN WO200240499-A1.				
PD 23-MAY-2002.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 5;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 927				
ID ABU07972 standard; protein; 932 AA.				
DE Human PMS1 protein.				
PN WO2003012130-A1.				
PD 13-FEB-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 928				
ID ABU07971 standard; protein; 932 AA.				
DE Human PMS2 protein.				
PN WO2003012130-A1.				
PD 13-FEB-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 929				
ID ABU89659 standard; protein; 932 AA.				
DE Human PMS2 mismatch repair protein.				
PN WO2003031937-A2.				
PD 17-APR-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 930				
ID ABU89660 standard; protein; 932 AA.				
DE Human PMS1 mismatch repair protein.				
PN WO2003031937-A2.				
PD 17-APR-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 931				
ID ABO07415 standard; protein; 932 AA.				
DE Human Mult. homologue, hMLH2.				
PN US2003027177-A1.				
PD 06-FEB-2003.				
PA (HUMA-) HUMAN GENOME SCT INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 932				
ID AAO27514 standard; protein; 932 AA.				
DE Human mismatch repair protein PMS (post meiotic segregation) 2				
PN WO2003062435-A1.				
PD 31-JUL-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 933				
ID AAO27515 standard; protein; 932 AA.				
DE Human mismatch repair protein PMS (post meiotic segregation) 1.				
PN WO2003062435-A1.				
PD 31-JUL-2003.				
PA (MORP-) MORPHOTEK INC.				
Query Match	12.5%;	Score 63;	DB 6;	Length 932;
Best Local Similarity	26.3%;	Pred. No. 9.3e+02;		
RESULT 934				
ID ADA06246 standard; protein; 932 AA.				
DE Human mismatch repair, MMR, protein PMS1.				
PN US2003068808-A1.				
PD 10-APR-2003.				
PA (NTCO/) NICOLAIDES N C.				
PA (SASS/) SASS P M.				

PA	(GRAS/) GRASSO L.
PB	(KLIN/) KLINIE J B.
Query Match	12.5%; Score 63; DB 7; Length 932
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 935	
ID	ADA06244 standard; protein; 932 AA.
DE	Human mismatch repair, MMR, protein PMS2.
PN	US2003068808-A1.
PD	10-APR-2003.
PA	(NICO/) NICOLAIDES N C.
PB	(SASS/) SASS P M.
PA	(GRAS/) GRASSO L.
PA	(KLIN/) KLINIE J B.
Query Match	12.5%; Score 63; DB 7; Length 932.
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 936	
ID	ADC09605 standard; protein; 932 AA.
DE	Human PMS2 protein SEQ ID NO:5.
PN	WO2003072732-A2.
PD	04-SEP-2003.
PA	(MORP-) MORPHOTEK INC.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 937	
ID	ADPC0607 standard; protein; 932 AA.
DE	Human PMS1 protein SEQ ID NO:7.
PN	WO2003072732-A2.
PD	04-SEP-2003.
PA	(MORP-) MORPHOTEK INC.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 938	
ID	ADPF1892 standard; protein; 932 AA.
DE	Human PMS1 protein, a mismatch repair protein.
PN	US6576468-B1.
PD	10-JUN-2003.
PA	(MORP-) MORPHOTEK INC.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 939	
ID	ADG62881 standard; protein; 932 AA.
DE	Human PMS2 protein.
PN	US2003165468-A1.
PD	04-SEP-2003.
PA	(GRAS/) GRASSO L.
PA	(NICO/) NICOLAIDES N C.
PA	(SASS/) SASS P M.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 940	
ID	ADG62882 standard; protein; 932 AA.
DE	Human PMS1 protein.
PN	US2003165468-A1.
PD	04-SEP-2003.
PA	(GRAS/) GRASSO L.
PA	(NICO/) NICOLAIDES N C.
PA	(SASS/) SASS P M.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 941	
ID	ADH62629 standard; protein; 932 AA.
DE	Human mismatch repair protein PMS1.
PN	US2003143682-A1.
PD	31-JUL-2003.
PA	(NICO/) NICOLAIDES N C.
PA	(GRAS/) GRASSO L.
PA	(SASS/) SASS P M.
Query Match	12.5%; Score 63; DB 7; Length 932;
Best Local Similarity	26.3%; Pred. No. 9.3e+02;
RESULT 942	
ID	ADH60983 standard; protein; 932 AA.
DE	Human mismatch repair protein hMLH2.
PN	US6610477-B1.

PD 26-AUG-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 12.5%; Score 63; DB 7; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 943
ID ADJ68675 standard; protein; 932 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID481.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.5%; Score 63; DB 7; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 944
ID ADF78840 standard; protein; 932 AA.
DE Human mismatch repair protein PMS1, cDNA.
PN US2003186441-A1.
PD 02-OCT-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 945
ID ADG46767 standard; protein; 932 AA.
DE Human MMR protein (mismatch protein), PMS1.
PN US2003091997-A1.
PD 15-MAY-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 946
ID ADO40066 standard; protein; 932 AA.
DE Human PMS1 protein.
PN US6737268-B1.
PD 18-MAY-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 947
ID ADP66682 standard; protein; 932 AA.
DE Human mismatch repair protein PMS2.
PN W02004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 948
ID ADP66680 standard; protein; 932 AA.
DE Human mismatch repair protein PMS1.
PN W02004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 949
ID ADR13883 standard; protein; 932 AA.
DE Human DNA mismatch repair protein PMS1.
PN US2004158886-A1.
PD 12-AUG-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 12.5%; Score 63; DB 8; Length 932;
Best Local Similarity 26.3%; Pred. No. 9.3e+02;
RESULT 950
ID ADP31471 standard; protein; 960 AA.
DE Human secreted protein SEQ ID #2238.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.5%; Score 63; DB 8; Length 960;

Best Local Similarity 35.7%; Pred. No. 9.6e+02;
RESULT 951
ID ADP31470 standard; protein; 960 AA.
DE Human secreted protein SEQ ID #2237.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.5%; Score 63; DB 8; Length 960;
Best Local Similarity 35.7%; Pred. No. 9.6e+02;
RESULT 952
ID ABB60399 standard; protein; 985 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7989.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.5%; Score 63; DB 4; Length 985;
Best Local Similarity 42.1%; Pred. No. 1e+03;
RESULT 953
ID ABB57807 standard; protein; 1007 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 213.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.5%; Score 63; DB 4; Length 1007;
Best Local Similarity 23.6%; Pred. No. 1e+03;
RESULT 954
ID AAG65895 standard; protein; 1062 AA.
DE Amino acid sequence of GSK gene Id 97078.
PN W0200172961-A2.
PD 04-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 12.5%; Score 63; DB 4; Length 1062;
Best Local Similarity 27.8%; Pred. No. 1.1e+03;
RESULT 955
ID AA017856 standard; protein; 1062 AA.
DE Pyrin domain containing protein NALP2/PY7-hs.
PN W0200240668-A2.
PD 23-MAY-2002.
PA (APOT-) APOTTECH RES & DEV LTD.
Query Match 12.5%; Score 63; DB 5; Length 1062;
Best Local Similarity 27.8%; Pred. No. 1.1e+03;
RESULT 956
ID ADM25903 standard; protein; 1299 AA.
DE Hyperthermophile Methanopyrus kandleri protein #509.
PN W02003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALV/) MALYKH A.
Query Match 12.5%; Score 63; DB 7; Length 1299;
Best Local Similarity 28.4%; Pred. No. 1.4e+03;
RESULT 957
ID AAY53970 standard; protein; 1857 AA.
DE Human peripheral benzodiazepine receptor associated protein-1.
PN W09960117-A2.
PD 25-NOV-1999.
PA (SNFI) SANOFI-SYNTHELABO.
Query Match 12.5%; Score 63; DB 3; Length 1857;
Best Local Similarity 28.8%; Pred. No. 2.3e+03;
RESULT 958
ID ADK40938 standard; protein; 3913 AA.
DE Novel human kinase protein #45.
PN W02003057841-A2.
PD 17-JUL-2003.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Query Match 12.5%; Score 63; DB 7; Length 3913;
Best Local Similarity 26.2%; Pred. No. 6.1e+03;
RESULT 959
ID ADR15659 standard; protein; 3913 AA.
DE Kinase 51594 1 hCT33056 1, SEQ ID 52.
PN W02004069154-A2.
PD 19-AUG-2004.

Query Match	12.5%;	Score 62.5;	DB 7;	Length 289;
Best Local Similarity	23.9%;	Pred. No. 2.3e+02;		
RESULT 969				
ID AAE01780 standard; protein; 302 AA.				
DE Human gene 11 encoded secreted protein HMBPE57, SEQ ID NO:101.				
PN W0200144627-A1.				
PD 17-MAY-2001.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%; <td>Score 62.5; <td>DB 4; <td>Length 302;</td> </td></td>	Score 62.5; <td>DB 4; <td>Length 302;</td> </td>	DB 4; <td>Length 302;</td>	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 970				
ID ABG64161 standard; protein; 302 AA.				
DE Human albumin fusion protein #836.				
PN W0200177137-A1.				
PD 18-OCT-2001.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%; <td>Score 62.5; <td>DB 5; <td>Length 302;</td> </td></td>	Score 62.5; <td>DB 5; <td>Length 302;</td> </td>	DB 5; <td>Length 302;</td>	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 971				
ID ADA57295 standard; protein; 302 AA.				
DE Human secreted protein #578.				
PN W02002102994-A2.				
PD 27-DEC-2002.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%; <td>Score 62.5; <td>DB 6; <td>Length 302;</td> </td></td>	Score 62.5; <td>DB 6; <td>Length 302;</td> </td>	DB 6; <td>Length 302;</td>	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 972				
ID ADA41174 standard; protein; 302 AA.				
DE Human secreted protein.				
PN W02002102993-A2.				
PD 27-DEC-2002.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%; <td>Score 62.5; <td>DB 6; <td>Length 302;</td> </td></td>	Score 62.5; <td>DB 6; <td>Length 302;</td> </td>	DB 6; <td>Length 302;</td>	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 973				
ID ADL77426 standard; protein; 302 AA.				
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 908.				
PN US2004010134-A1.				
PD 15-JAN-2004.				
PA (ROSE/) ROSEN C A.				
PA (HASE/) HASELTINE W A.				
Query Match	12.5%; <td>Score 62.5; <td>DB 8; <td>Length 302;</td> </td></td>	Score 62.5; <td>DB 8; <td>Length 302;</td> </td>	DB 8; <td>Length 302;</td>	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 974				
ID AAG65717 standard; protein; 361 AA.				
DE A. goseypil AG008 gene product.				
PN US6291665-B1.				
PD 18-SEP-2001.				
PA (SYGN) SYNGENTA PARTICIPATIONS AG.				
Query Match	12.5%; <td>Score 62.5; <td>DB 4; <td>Length 361;</td> </td></td>	Score 62.5; <td>DB 4; <td>Length 361;</td> </td>	DB 4; <td>Length 361;</td>	Length 361;
Best Local Similarity	34.5%;	Pred. No. 3e+02;		
RESULT 975				
ID ADS15031 standard; protein; 401 AA.				
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 586				
PN W02000408385-A2.				
PD 30-SEP-2004.				
PA (IOWA) UNIV IOWA RES FOUND.				
Query Match	12.5%; <td>Score 62.5; <td>DB 8; <td>Length 401;</td> </td></td>	Score 62.5; <td>DB 8; <td>Length 401;</td> </td>	DB 8; <td>Length 401;</td>	Length 401;
Best Local Similarity	31.0%;	Pred. No. 3.5e+02;		
RESULT 976				
ID AAG44543 standard; protein; 426 AA.				
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55809.				
PN EPI0133405-A2.				
PD 06-SEP-2000.				
Query Match	12.5%; <td>Score 62.5; <td>DB 3; <td>Length 426;</td> </td></td>	Score 62.5; <td>DB 3; <td>Length 426;</td> </td>	DB 3; <td>Length 426;</td>	Length 426;
Best Local Similarity	29.5%;	Pred. No. 3.8e+02;		
RESULT 977				
ID ABB91634 standard; protein; 426 AA.				
DE Herbicidially active polypeptide SEQ ID NO 845.				
PN W0200210210-A2.				
PD 07-FEB-2002.				
PA (PAPP) PAPP INC				

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Best Local Similarity 29.5%; Pred. No. 3.8e+02;
RESULT 978
ID ABU26371 standard; protein; 445 AA.
DE Protein encoded by prokaryotic essential gene #11898.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 62.5; DB 6; Length 445;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 979
ID ABU33109 standard; protein; 471 AA.
DE Protein encoded by prokaryotic essential gene #18636.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 62.5; DB 6; Length 471;
Best Local Similarity 29.7%; Pred. No. 4.3e+02;
RESULT 980
ID ABB71148 standard; protein; 505 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40236.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (BEKE-) BE CORP NY.
Query Match 12.5%; Score 62.5; DB 4; Length 505;
Best Local Similarity 28.8%; Pred. No. 4.7e+02;
RESULT 981
ID ADS27978 standard; protein; 511 AA.
DE Bacterial polypeptide #17011.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 511;
Best Local Similarity 28.3%; Pred. No. 4.8e+02;
RESULT 982
ID ABB57291 standard; protein; 560 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:819.
PN W0200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 12.5%; Score 62.5; DB 5; Length 560;
Best Local Similarity 29.6%; Pred. No. 5.4e+02;
RESULT 983
ID ADO80490 standard; protein; 573 AA.
DE Deinococcus radiodurans mety protein.
PN DE10239082-A1.
PD 04-MAR-2004.
PA (BADI-) BASF AG.
Query Match 12.5%; Score 62.5; DB 8; Length 573;
Best Local Similarity 32.9%; Pred. No. 5.6e+02;
RESULT 984
ID ADN17889 standard; protein; 573 AA.
DE Bacterial polypeptide #542.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 573;
Best Local Similarity 32.9%; Pred. No. 5.6e+02;
RESULT 985
ID ADM99207 standard; protein; 596 AA.
DE Environmentally sourced protease protein Segid 90.
PN W02004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 12.5%; Score 62.5; DB 8; Length 596;
Best Local Similarity 29.5%; Pred. No. 5.9e+02;

Best Local Similarity 29.5%; Pred. No. 5.9e+02;
RESULT 986
ID ADN18270 standard; protein; 601 AA.
DE Bacterial polypeptide #923.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 601;
Best Local Similarity 28.7%; Pred. No. 5.9e+02;
RESULT 987
ID ADG31175 standard; protein; 615 AA.
DE Fruit fly cpo protein.
PN W02003092715-A2.
PD 13-NOV-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 12.5%; Score 62.5; DB 7; Length 615;
Best Local Similarity 28.8%; Pred. No. 6.1e+02;
RESULT 988
ID ADS14849 standard; protein; 618 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 404.
PN W02004083385-A2.
PD 30-SEP-2004.
PA (IOWA-) UNIV IOWA RES FOUND.
Query Match 12.5%; Score 62.5; DB 8; Length 618;
Best Local Similarity 27.8%; Pred. No. 6.1e+02;
RESULT 989
ID AAE18906 standard; protein; 643 AA.
DE Human PAS domain protein (PASDP-1).
PN W0200210200-A2.
PD 07-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 62.5; DB 5; Length 643;
Best Local Similarity 50.0%; Pred. No. 6.5e+02;
RESULT 990
ID AAU62829 standard; protein; 652 AA.
DE Propionibacterium acnes immunogenic protein #23725.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 4; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 991
ID AAM59348 standard; protein; 652 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #24024.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 992
ID AAM65103 standard; protein; 652 AA.
DE Propionibacterium acnes immunogenic polypeptide #29779.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 993
ID AAM69757 standard; protein; 802 AA.
DE Acetobacter xylinum bcsb gene product.
PN W09839455-A1.
PD 11-SEP-1998.
PA (BIOP-) BIO-POLYMER RES CO LTD.
Query Match 12.5%; Score 62.5; DB 2; Length 802;
Best Local Similarity 26.4%; Pred. No. 8.7e+02;
RESULT 994
ID AAO18572 standard; protein; 802 AA.
DE Rat transcriptional regulatory factor.
PN W0200253735-A1.
PD 11-JUL-2002.
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PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 995
ID AAO18571 standard; protein; 802 AA.
DE Murine transcriptional regulatory factor.
PN WO200253735-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 996
ID AAO18570 standard; protein; 802 AA.
DE Human transcriptional regulatory factor.
PN WO200253735-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 997
ID AAO18254 standard; protein; 802 AA.
DE Murine basic helix-loop-helix BHLH-PAS protein.
PN WO200253729-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 998
ID AAO18255 standard; protein; 802 AA.
DE Rat basic helix-loop-helix BHLH-PAS protein.
PN WO200253729-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 999
ID AAO18253 standard; protein; 802 AA.
DE Human basic helix-loop-helix BHLH-PAS protein.
PN WO200253729-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1000
ID ABB81802 standard; protein; 802 AA.
DE Rat transcriptional regulator.
PN WO200253736-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1001
ID ABB81800 standard; protein; 802 AA.
DE Human transcriptional regulator.
PN WO200253736-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1002
ID ABB81801 standard; protein; 802 AA.
DE Mouse transcriptional regulator.
PN WO200253736-A1.
PD 11-JUL-2002.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 12.5%; Score 62.5; DB 5; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1003
ID ADD31213 standard; protein; 802 AA.
DE Variant of rat K11 polypeptide.
PN US2003190653-A1.
PD 09-OCT-2003.
PA (SHAM/) SHAWLOO M.

PA (GONZ/) GONZALEZ-ZULUETA M.
Query Match 12.5%; Score 62.5; DB 7; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1004
ID ADD31203 standard; protein; 802 AA.
DE Human K11 polypeptide.
PN US2003190653-A1.
PD 09-OCT-2003.
PA (SHAM/) SHAWLOO M.
PA (GONZ/) GONZALEZ-ZULUETA M.
PA (WTEL/) WIELOCH T.
Query Match 12.5%; Score 62.5; DB 7; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1005
ID ADD31201 standard; protein; 802 AA.
DE Rat K11 polypeptide.
PN US2003190653-A1.
PD 09-OCT-2003.
PA (SHAM/) SHAWLOO M.
PA (GONZ/) GONZALEZ-ZULUETA M.
PA (WTEL/) WIELOCH T.
Query Match 12.5%; Score 62.5; DB 7; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1006
ID ADM04925 standard; protein; 802 AA.
DE Human protein of the invention SEQ ID NO:3610.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.5%; Score 62.5; DB 7; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1007
ID ADJ37241 standard; protein; 802 AA.
DE Human nucleic-acid associated protein NNAIP-30 SEQ ID NO:30.
PN WO2004011604-A2.
PD 05-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.5%; Score 62.5; DB 8; Length 802;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1008
ID ABO62421 standard; protein; 922 AA.
DE Klebsiella pneumoniae polypeptide seqid 8938.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 7; Length 922;
Best Local Similarity 29.6%; Pred. No. 1e+03;
RESULT 1009
ID ADE08640 standard; protein; 967 AA.
DE Novel protein (useful for identifying genetic disorders) #795.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 62.5; DB 7; Length 967;
Best Local Similarity 31.1%; Pred. No. 1.1e+03;
RESULT 1010
ID ABB69643 standard; protein; 970 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35721.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERK-) PER CORP NY.
Query Match 12.5%; Score 62.5; DB 4; Length 970;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
RESULT 1011
ID AAB23249 standard; protein; 999 AA.
DE Streptomyces collinus Ansd/Ansk protein.
PN WO200055304-A2.
PD 21-SEP-2000.
PA (UTVI-) UNIV VIRGINIA COMMONWEALTH.
Query Match 12.5%; Score 62.5; DB 3; Length 999;
Best Local Similarity 29.3%; Pred. No. 1.2e+03;
RESULT 1012

ID ADC13549 standard; protein; 1149 AA.
DE Human NOVX protein, SEQ ID No 28.
PN WO2003004617-A2.
PD 16-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.5%; Score 62.5; DB 7; Length 1149;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1013
ID ABB62191 standard; protein; 1224 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13365.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.5%; Score 62.5; DB 4; Length 1224;
Best Local Similarity 27.6%; Pred. No. 1.5e+03;
RESULT 1014
ID ABO75059 standard; protein; 1626 AA.
DE Pseudomonas aeruginosa polypeptide #7234.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 7; Length 1626;
Best Local Similarity 25.3%; Pred. No. 2.2e+03;
RESULT 1015
ID AAU04484 standard; protein; 1873 AA.
DE Human PD-ATP-binding cassette (PD-ABC) protein form #2.
PN WO200153490-A1.
PD 26-JUL-2001.
PA (WARN) WARNER LAMBERT CO.
Query Match 12.5%; Score 62.5; DB 4; Length 1873;
Best Local Similarity 41.9%; Pred. No. 2.6e+03;
RESULT 1016
ID ABU08465 standard; protein; 1993 AA.
DE Amino acid sequence for human ABCA7 splice variant #2.
PN WO2003010315-A1.
PD 06-FEB-2003.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
Query Match 12.5%; Score 62.5; DB 6; Length 1993;
Best Local Similarity 41.9%; Pred. No. 2.9e+03;
RESULT 1017
ID ADP55322 standard; protein; 2000 AA.
DE Human PRO protein sequence SEQ ID NO:1298.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 62.5; DB 8; Length 2000;
Best Local Similarity 41.9%; Pred. No. 2.9e+03;
RESULT 1018
ID ABU08464 standard; protein; 2008 AA.
DE Amino acid sequence for human ABCA7 splice variant #1.
PN WO2003010315-A1.
PD 06-FEB-2003.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
Query Match 12.5%; Score 62.5; DB 6; Length 2008;
Best Local Similarity 41.9%; Pred. No. 2.9e+03;
RESULT 1019
ID ABU54629 standard; protein; 2059 AA.
DE Human NOVX polypeptide #88.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 2059;
Best Local Similarity 41.9%; Pred. No. 3e+03;
RESULT 1020
ID ABG20760 standard; protein; 2120 AA.
DE Novel human diagnostic protein #20751.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 62.5; DB 4; Length 2120;
Best Local Similarity 26.6%; Pred. No. 3.1e+03;

RESULT 1021
ID AAU04483 standard; protein; 2146 AA.
DE Human PD-ATP-binding cassette (PD-ABC) protein form #1.
PN WO200153490-A1.
PD 26-JUL-2001.
PA (WARN) WARNER LAMBERT CO.
Query Match 12.5%; Score 62.5; DB 4; Length 2146;
Best Local Similarity 41.9%; Pred. No. 3.2e+03;
RESULT 1022
ID ABP52096 standard; protein; 2146 AA.
DE Homo sapiens ABC transporter ABCA7 protein SEQ ID NO:48.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 12.5%; Score 62.5; DB 5; Length 2146;
Best Local Similarity 41.9%; Pred. No. 3.2e+03;
RESULT 1023
ID ABU08466 standard; protein; 2146 AA.
DE Human ABCA-SSN protein.
PN WO2003010315-A1.
PD 06-FEB-2003.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
Query Match 12.5%; Score 62.5; DB 6; Length 2146;
Best Local Similarity 41.9%; Pred. No. 3.2e+03;
RESULT 1024
ID ABG72696 standard; protein; 2146 AA.
DE Human ATP-binding cassette transporter-like protein, ABCL.
PN US2002127647-A1.
PD 12-SEP-2002.
PA (SHUT/) SHUTTER J.
PA (ULIA/) ULIAS L.
Query Match 12.5%; Score 62.5; DB 6; Length 2146;
Best Local Similarity 41.9%; Pred. No. 3.2e+03;
RESULT 1025
ID AAO14210 standard; protein; 2180 AA.
DE Human transporter and ion channel TRICH-27.
PN WO2002045520-A2.
PD 17-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 62.5; DB 5; Length 2180;
Best Local Similarity 41.9%; Pred. No. 3.2e+03;
RESULT 1026
ID ABB81459 standard; protein; 2541 AA.
DE Human Talin protein SEQ ID NO:3.
PN US6372492-B1.
PD 16-APR-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 12.5%; Score 62.5; DB 5; Length 2541;
Best Local Similarity 24.3%; Pred. No. 3.9e+03;
RESULT 1027
ID ADG90450 standard; protein; 2541 AA.
DE Human talin.
PN WO200268446-A1.
PD 06-SEP-2002.
PA (ISIS-) ISIS PHARM INC.
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
Query Match 12.5%; Score 62.5; DB 5; Length 2541;
Best Local Similarity 24.3%; Pred. No. 3.9e+03;
RESULT 1028
ID ABR47614 standard; protein; 2541 AA.
DE Breast cancer associated protein sequence SEQ ID NO:470.
PN WO2003004989-A2.
PD 16-JUN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 12.5%; Score 62.5; DB 6; Length 2541;
Best Local Similarity 24.3%; Pred. No. 3.9e+03;
RESULT 1029
ID ADP85745 standard; protein; 2541 AA.
DE Human Talin protein.
PN US2004110705-A1.
PD 10-JUN-2004.
PA (BENN/) BENNETT C F.

PA (COWS/) COMSERT L M.
Query Match 12.5%; Score 62.5; DB 8; Length 2541;
Best Local Similarity 24.3%; Pred. No. 3.9e+03;
RESULT 1030
ID AAM56448 standard; protein; 2723 AA.
DE Fragment Hgu1775 of a new Hepatitis virus g protein.
PN UPI0108685-A.
PD 28-APR-1998.
PA (BMLB-) BML KK.
Query Match 12.5%; Score 62.5; DB 2; Length 2723;
Best Local Similarity 27.1%; Pred. No. 4.3e+03;
RESULT 1031
ID AAM27227 standard; protein; 2861 AA.
DE Human TRIO phosphoprotein.
PN W09735979-A1.
PD 02-OCT-1997.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 12.5%; Score 62.5; DB 2; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1032
ID ABG17024 standard; protein; 2861 AA.
DE Novel human diagnostic protein #17015.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 62.5; DB 4; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1033
ID AAG68192 standard; protein; 2861 AA.
DE GTPase protein SEQ ID NO:108.
PN W0200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 4; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1034
ID ABR41116 standard; protein; 2861 AA.
DE Human GTPase gene TRIO protein product.
PN W0200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1035
ID ABU70968 standard; protein; 2861 AA.
DE Human adipocyte Selected Interacting domain, SID, #599.
PN W0200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.5%; Score 62.5; DB 6; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1036
ID ADB98736 standard; protein; 2861 AA.
DE Human GTPase.
PN W0200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 7; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1037
ID ADE82532 standard; protein; 2861 AA.
DE Human protein sequence related to the invention #22.
PN W0200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 62.5; DB 7; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1038
ID ADD89085 standard; protein; 2861 AA.
DE TAT288.
PA (AMHP) WYETH.
Query Match 12.5%; Score 62.5; DB 7; Length 2861;
Best Local Similarity 26.6%; Pred. No. 4.6e+03;
RESULT 1039
ID AAM70262 standard; protein; 111 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30568.
PN W0200157276-A2.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1040
ID ABB31885 standard; peptide; 111 AA.
DE Peptide #4536 encoded by breast cell single exon nucleic acid probe.
PN W0200157271-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1041
ID ABB31885 standard; peptide; 111 AA.
DE Peptide #4536 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1042
ID AAM18090 standard; protein; 111 AA.
DE Peptide #4524 encoded by probe for measuring cervical gene expression.
PN W0200157278-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1043
ID ABB37124 standard; peptide; 111 AA.
DE Peptide #4630 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1044
ID AAM30600 standard; protein; 111 AA.
DE Peptide #4637 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1045
ID ABB31885 standard; peptide; 111 AA.
DE Peptide #4536 encoded by breast cell single exon nucleic acid probe.
PN W0200157271-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1046
ID ABB22436 standard; protein; 111 AA.
DE Protein #4435 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLF-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1047
ID AAM70262 standard; protein; 111 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30568.
PN W0200157276-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1048
ID AAM57845 standard; protein; 111 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29950.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1049
ID ABG51959 standard; peptide; 111 AA.
DE Human liver peptide, SEQ ID No 30607.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1050
ID AAM05724 standard; protein; 111 AA.
DE Peptide #4406 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 4; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1051
ID ABG39904 standard; peptide; 111 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29569.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.4%; Score 62; DB 5; Length 111;
Best Local Similarity 31.2%; Pred. No. 73;
RESULT 1052
ID AAY19666 standard; protein; 123 AA.
DE SEQ ID NO 384 from W09922243.
PN W09922243-A1.
PD 06-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.4%; Score 62; DB 2; Length 123;
Best Local Similarity 28.6%; Pred. No. 84;
RESULT 1053
ID AAG90290 standard; protein; 128 AA.
DE C glutamicum protein fragment SEQ ID NO: 4044.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOM-) KYOMA HAKKO KOGYO KK.
Query Match 12.4%; Score 62; DB 4; Length 128;
Best Local Similarity 30.9%; Pred. No. 88;
RESULT 1054
ID ABG73369 standard; protein; 280 AA.
DE Murine ischaemia activated protein (IAP).
PN US2002160495-A1.
PD 31-OCT-2002.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 12.4%; Score 62; DB 6; Length 280;
Best Local Similarity 25.6%; Pred. No. 2.5e+02;
RESULT 1055
ID AAE20090 standard; protein; 289 AA.
DE Lactobacillus rhamnosus serine dehydratase alpha subunit (sdha).
PN W0200212506-A1.
PD 14-FEB-2002.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.4%; Score 62; DB 5; Length 289;
Best Local Similarity 32.8%; Pred. No. 2.6e+02;
RESULT 1056
ID ABO82283 standard; protein; 312 AA.
DE Pseudomonas aeruginosa polypeptide #14458.
PN US6551795-B1.

PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 62; DB 7; Length 312;
Best Local Similarity 30.3%; Pred. No. 2.8e+02;
RESULT 1057
ID ABU3983 standard; protein; 322 AA.
DE Protein encoded by Prokaryotic essential gene #19510.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.4%; Score 62; DB 6; Length 322;
Best Local Similarity 28.9%; Pred. No. 3e+02;
RESULT 1058
ID ABO70710 standard; protein; 336 AA.
DE Pseudomonas aeruginosa polypeptide #2885.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 62; DB 7; Length 336;
Best Local Similarity 26.8%; Pred. No. 3.1e+02;
RESULT 1059
ID ABO78853 standard; protein; 372 AA.
DE Pseudomonas aeruginosa polypeptide #11028.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 62; DB 7; Length 372;
Best Local Similarity 26.3%; Pred. No. 3.6e+02;
RESULT 1060
ID ABB58579 standard; protein; 393 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2529.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.4%; Score 62; DB 4; Length 393;
Best Local Similarity 25.9%; Pred. No. 3.9e+02;
RESULT 1061
ID ADS21653 standard; protein; 393 AA.
DE Bacterial polypeptide #10686.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.4%; Score 62; DB 8; Length 393;
Best Local Similarity 34.5%; Pred. No. 3.9e+02;
RESULT 1062
ID ABO60011 standard; protein; 408 AA.
DE Human genome derived single exon protein #6245.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENNN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.4%; Score 62; DB 8; Length 408;
Best Local Similarity 25.3%; Pred. No. 4.1e+02;
RESULT 1063
ID ABO71750 standard; protein; 444 AA.
DE Pseudomonas aeruginosa polypeptide #3925.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 62; DB 7; Length 444;
Best Local Similarity 27.3%; Pred. No. 4.5e+02;
RESULT 1064
ID ABO74128 standard; protein; 468 AA.
DE Pseudomonas aeruginosa polypeptide #6303.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 62; DB 7; Length 468;

Best Local Similarity 27.6%; Pred. No. 4.9e+02;
RESULT 1065
ID ABU49789 standard; protein; 474 AA.
DE Human novel protein encoded by Prokaryotic essential gene #35316.
PN WO2002727183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 28.8%; Pred. No. 4.9e+02; Length 474;
RESULT 1066
ID ABO63015 standard; protein; 484 AA.
DE Klebsiella pneumoniae polypeptide seqid 9532.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 25.5%; Pred. No. 5.1e+02; Length 484;
RESULT 1067
ID ABO63222 standard; protein; 528 AA.
DE Klebsiella pneumoniae polypeptide seqid 9739.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 29.5%; Pred. No. 5.7e+02; Length 528;
RESULT 1068
ID ADG47934 standard; protein; 549 AA.
DE Beta-vulgaris-like sugar transport protein #1.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE-) HELENTJARIS T G.
Query Match
Best Local Similarity 22.7%; Pred. No. 6e+02; Length 549;
RESULT 1069
ID ADS24035 standard; protein; 549 AA.
DE Bacterial polypeptide #13068.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 27.3%; Pred. No. 6e+02; Length 549;
RESULT 1070
ID ABU41401 standard; protein; 559 AA.
DE Protein encoded by Prokaryotic essential gene #26928;
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 6.1e+02; Length 559;
RESULT 1071
ID ABB65575 standard; protein; 574 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23517.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 32.8%; Pred. No. 6.3e+02; Length 574;
RESULT 1072
ID ADQ03088 standard; protein; 574 AA.
DE P. aeruginosa virulence gene, VIR18, protein.
PN US2004122212-A1.
PD 24-JUN-2004.
PA (COSS/) COSSON P.
PA (KOHL/) KOHLER T.
PA (BENG/) BENGEZAI M.
PA (MARC/) MARCHETTI A.
PA (DELD/) DELDEN C V.
Query Match
Best Local Similarity 27.3%; Pred. No. 6.3e+02; Length 574;
Score 62; DB 8; Length 574;
Score 62; DB 8; Length 574;
Score 62; DB 8; Length 574;

RESULT 1073
ID ABU65064 standard; protein; 616 AA.
DE Human NOVI14c protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02; Length 616;
RESULT 1074
ID ABU65063 standard; protein; 616 AA.
DE Human NOVI14b protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02; Length 616;
RESULT 1075
ID ADK51048 standard; protein; 616 AA.
DE Human NOVI18A protein sequence SeqID68.
PN WO2003083046-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02; Length 616;
RESULT 1076
ID ADH42447 standard; protein; 616 AA.
DE Novel human protein NOV67d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02; Length 616;
RESULT 1077
ID ADN61777 standard; protein; 616 AA.
DE Human novel protein NOVI14b.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOV S G.
PA (TAUP/) TAUPFER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERR/) ZERRHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KERU/) KERUDA R.
PA (PART/) PARTURAJAN M.
PA (GANG/) GANGOLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASHMAN S J.
PA (MALY/) MALYANKAR V M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02; Length 616;
RESULT 1078
ID ADN61779 standard; protein; 616 AA.
DE Human novel protein NOVI14c.

PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENNA/) PENNA C E A.
PA (LILL/) LI L.
PA (ZERN/) ZERHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (UTIM/) JT W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHER/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASW/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LITY/) LITV Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURESS C B.
Query Match 12.4%; Score 62; DB 8; Length 616;
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1079
ID ADS96436 standard; protein; 637 AA.
DE Drosophila melanogaster protein, SEQ ID 57.
PN WO200403999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.4%; Score 62; DB 8; Length 637;
Best Local Similarity 32.0%; Pred. No. 7.3e+02;
RESULT 1080
ID ADS27839 standard; protein; 643 AA.
DE Bacterial polypeptide #16872.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.4%; Score 62; DB 8; Length 643;
Best Local Similarity 28.0%; Pred. No. 7.4e+02;
RESULT 1081
ID ADC00466 standard; protein; 645 AA.
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 511.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 12.4%; Score 62; DB 7; Length 645;
Best Local Similarity 22.7%; Pred. No. 7.4e+02;
RESULT 1082
ID ADI45319 standard; protein; 649 AA.
DE Rice isoprenoid biosynthesis-associated protein #125.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUC/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 12.4%; Score 62; DB 8; Length 649;
Best Local Similarity 31.5%; Pred. No. 7.5e+02;
RESULT 1083
ID ADF74751 standard; protein; 671 AA.
DE Murine dnaform 41412 protein, an ATP binding cassette (SegID 30).
PN WO2003091435-A1.
PD 06-NOV-2003.
PA (RIKE) RIKEN KK.
PA (DNMF-) DNAFORM KK.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 12.4%; Score 62; DB 7; Length 671;
Best Local Similarity 39.5%; Pred. No. 7.8e+02;
RESULT 1084
ID ABB62230 standard; protein; 883 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13482.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.4%; Score 62; DB 4; Length 883;
Best Local Similarity 25.4%; Pred. No. 1.1e+03;
RESULT 1085
ID AAB42926 standard; protein; 903 AA.
DE Human ORFX ORF2690 polypeptide sequence SEQ ID NO:5380.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CUPA-) CUPAGEN CORP.
Query Match 12.4%; Score 62; DB 3; Length 903;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 1086
ID ADF69021 standard; protein; 903 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID827.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.4%; Score 62; DB 7; Length 903;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 1087
ID ABB97506 standard; protein; 966 AA.
DE Novel human protein SEQ ID NO: 774.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 62; DB 5; Length 966;
Best Local Similarity 25.3%; Pred. No. 1.3e+03;
RESULT 1088
ID ADJ70349 standard; protein; 966 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2155.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.4%; Score 62; DB 7; Length 966;
Best Local Similarity 25.3%; Pred. No. 1.3e+03;
RESULT 1089
ID ABU41551 standard; protein; 1215 AA.
DE Protein encoded by Prokaryotic essential gene #27078.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.4%; Score 62; DB 6; Length 1215;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
RESULT 1090
ID ADF74752 standard; protein; 1250 AA.
DE Murine dnaform 43395 protein, an ATP binding cassette (SegID 31).
PN WO2003091435-A1.

Best Local Similarity 32.0%; Pred. No. 2.8e+02;
RESULT 1106
ID AAB35598 standard; protein; 306 AA.
DE Haemophilus influenzae cellular proliferation protein #239.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 4; Length 306;
Best Local Similarity 31.6%; Pred. No. 3.2e+02;
RESULT 1107
ID AAB56999 standard; protein; 306 AA.
DE Haemophilus influenzae D-Ala-D-Ala ligase enzyme SEQ ID NO:5.
PN WO2003002063-A2.
PD 09-JAN-2003.
PA (ESSE-) ESSENTIAL THERAPEUTICS INC.
PA (PLIV) PLIVA DD ZAGREB.
Query Match 12.3%; Score 61.5; DB 6; Length 306;
Best Local Similarity 31.6%; Pred. No. 3.2e+02;
RESULT 1108
ID AAB0500 standard; protein; 306 AA.
DE Protein encoded by Prokaryotic essential gene #16027.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 306;
Best Local Similarity 31.6%; Pred. No. 3.2e+02;
RESULT 1109
ID AAB29367 standard; protein; 309 AA.
DE Novel human diagnostic protein #29358.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 61.5; DB 4; Length 309;
Best Local Similarity 30.6%; Pred. No. 3.2e+02;
RESULT 1110
ID AAB03955 standard; protein; 344 AA.
DE Human mesenchymal stem cell polypeptide.
PN WO200059933-A2.
PD 12-OCT-2000.
PA (OSIR-) OSIRIS THERAPEUTICS INC.
Query Match 12.3%; Score 61.5; DB 3; Length 344;
Best Local Similarity 32.0%; Pred. No. 3.7e+02;
RESULT 1111
ID AAB93360 standard; protein; 344 AA.
DE Human protein sequence SEQ ID NO:12497.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.3%; Score 61.5; DB 4; Length 344;
Best Local Similarity 32.0%; Pred. No. 3.7e+02;
RESULT 1112
ID AAB89632 standard; protein; 344 AA.
DE Human polypeptide SEQ ID NO 2008.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 61.5; DB 5; Length 344;
Best Local Similarity 32.0%; Pred. No. 3.7e+02;
RESULT 1113
ID ADJ69569 standard; protein; 344 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1375.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.3%; Score 61.5; DB 7; Length 344;
Best Local Similarity 32.0%; Pred. No. 3.7e+02;
RESULT 1114
ID ADS42410 standard; protein; 344 AA.
DE Bacterial polypeptide #20840.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 344;
Best Local Similarity 29.1%; Pred. No. 3.7e+02;
RESULT 1115
ID AAB18838 standard; protein; 350 AA.
DE Protein encoded by Prokaryotic essential gene #4365.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 350;
Best Local Similarity 30.8%; Pred. No. 3.8e+02;
RESULT 1116
ID AAB03935 standard; protein; 361 AA.
DE Novel human secreted protein #1426.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 61.5; DB 4; Length 361;
Best Local Similarity 25.6%; Pred. No. 3.9e+02;
RESULT 1117
ID AAB10101 standard; protein; 367 AA.
DE Human homeobox protein NKx6.1 amino acid sequence.
PN WO200218545-A1.
PD 07-MAR-2002.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 12.3%; Score 61.5; DB 5; Length 367;
Best Local Similarity 28.9%; Pred. No. 4e+02;
RESULT 1118
ID AAB70892 standard; protein; 367 AA.
DE Human NKX-6.1 protein.
PN US643667-B1.
PD 20-AUG-2002.
PA (REGC) UNIV CALIFORNIA.
PA (UNIW) UNIV WASHINGTON.
Query Match 12.3%; Score 61.5; DB 5; Length 367;
Best Local Similarity 28.9%; Pred. No. 4e+02;
RESULT 1119
ID ADQ09851 standard; protein; 367 AA.
DE Human NK-2 class homeobox protein, NKx6.1.
PN US2004132679-A1.
PD 08-JUL-2004.
PA (BAY) BAYLOR COLLEGE MEDICINE.
Query Match 12.3%; Score 61.5; DB 8; Length 367;
Best Local Similarity 28.9%; Pred. No. 4e+02;
RESULT 1120
ID AAU45721 standard; protein; 369 AA.
DE Propionibacterium acnes immunogenic protein #6617.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.3%; Score 61.5; DB 4; Length 369;
Best Local Similarity 27.4%; Pred. No. 4e+02;
RESULT 1121
ID ABM42240 standard; protein; 369 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6916.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.3%; Score 61.5; DB 6; Length 369;
Best Local Similarity 27.4%; Pred. No. 4e+02;
RESULT 1122
ID ADN25671 standard; protein; 378 AA.
DE Bacterial polypeptide #8324.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 12.3%; Score 61.5; DB 8; Length 378;
Best Local Similarity 30.6%; Pred. No. 4.2e+02;
RESULT 1123
ID ABB82801 standard; protein; 384 AA.
DE A. radiobacter Opda polypeptide mutant Opda2.
PN W0200292803-A1.
PD 21-NOV-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 12.3%; Score 61.5; DB 6; Length 384;
Best Local Similarity 32.9%; Pred. No. 4.3e+02;
RESULT 1124
ID ABB82798 standard; protein; 384 AA.
DE A. radiobacter Opda polypeptide.
PN W0200292803-A1.
PD 21-NOV-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 12.3%; Score 61.5; DB 6; Length 384;
Best Local Similarity 32.9%; Pred. No. 4.3e+02;
RESULT 1125
ID ABB82800 standard; protein; 384 AA.
DE A. radiobacter Opda polypeptide mutant Opda1.
PN W0200292803-A1.
PD 21-NOV-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 12.3%; Score 61.5; DB 6; Length 384;
Best Local Similarity 32.9%; Pred. No. 4.3e+02;
RESULT 1126
ID ADJ45734 standard; protein; 384 AA.
DE Agrobacterium radiobacter Opda protein SEQ ID NO:30.
PN W02004011492-A1.
PD 05-FEB-2004.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 12.3%; Score 61.5; DB 8; Length 384;
Best Local Similarity 32.9%; Pred. No. 4.3e+02;
RESULT 1127
ID ADN22118 standard; protein; 389 AA.
DE Bacterial polypeptide #4771.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 389;
Best Local Similarity 27.0%; Pred. No. 4.3e+02;
RESULT 1128
ID ADN24878 standard; protein; 392 AA.
DE Bacterial polypeptide #7531.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 392;
Best Local Similarity 27.0%; Pred. No. 4.4e+02;
RESULT 1129
ID AD623141 standard; protein; 422 AA.
DE Bacterial polypeptide #12174.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 422;
Best Local Similarity 29.3%; Pred. No. 4.8e+02;
RESULT 1130
ID ADN19902 standard; protein; 428 AA.
DE Bacterial polypeptide #2555.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 428;
Best Local Similarity 24.5%; Pred. No. 4.9e+02;
RESULT 1131
ID ABU25929 standard; protein; 431 AA.
DE Protein encoded by Prokaryotic essential gene #11456.
PN W0200077183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 431;
Best Local Similarity 26.7%; Pred. No. 5e+02;
RESULT 1132
ID AAM12400 standard; protein; 433 AA.
DE A. chrysoeum O-acetylhomoserine sulphydrylase protein.
PN JF08336391-A.
PD 24-DEC-1996.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 12.3%; Score 61.5; DB 2; Length 433;
Best Local Similarity 28.0%; Pred. No. 5e+02;
RESULT 1133
ID AAG81144 standard; protein; 441 AA.
DE Mycobacterium tuberculosis potential drug target protein SEQ ID 195.
PN W0200135317-A1.
PD 17-MAY-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 12.3%; Score 61.5; DB 4; Length 441;
Best Local Similarity 24.5%; Pred. No. 5.1e+02;
RESULT 1134
ID ABP57503 standard; protein; 441 AA.
DE Mycobacterium tuberculosis protein SEQ ID NO:135.
PN W0200300721-A2.
PD 03-JAN-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 12.3%; Score 61.5; DB 6; Length 441;
Best Local Similarity 24.5%; Pred. No. 5.1e+02;
RESULT 1135
ID ABU24297 standard; protein; 447 AA.
DE Protein encoded by Prokaryotic essential gene #9824.
PN W020027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 447;
Best Local Similarity 28.4%; Pred. No. 5.2e+02;
RESULT 1136
ID AB079444 standard; protein; 447 AA.
DE Pseudomonas aeruginosa polypeptide #11619.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.3%; Score 61.5; DB 7; Length 447;
Best Local Similarity 25.6%; Pred. No. 5.2e+02;
RESULT 1137
ID AD139278 standard; protein; 476 AA.
DE S. hygroscopicus geldanamycin gene cluster-encoded protein, SEQ ID:120.
PN W02003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Query Match 12.3%; Score 61.5; DB 8; Length 476;
Best Local Similarity 31.6%; Pred. No. 5.6e+02;
RESULT 1138
ID ABO62871 standard; protein; 578 AA.
DE Klebsiella pneumoniae polypeptide seqid 9388.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.3%; Score 61.5; DB 7; Length 578;

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Best Local Similarity 23.8%; Pred. No. 7.3e+02;
RESULT 1139
ID ADN18902 standard; protein; 587 AA.
DE Bacterial polypeptide #1555.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 587;
Best Local Similarity 27.5%; Pred. No. 7.4e+02;
RESULT 1140
ID ADJ87349 standard; protein; 630 AA.
DE DNA replication and pathogenesis associated protein RXA00157.
PN DE10154246-A1.
PD 08-MAY-2003.
PA (BADI ) BASF AG.
Query Match 12.3%; Score 61.5; DB 7; Length 630;
Best Local Similarity 27.1%; Pred. No. 8.2e+02;
RESULT 1141
ID ABU21547 standard; protein; 704 AA.
DE Protein encoded by Prokaryotic essential gene #7074.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 704;
Best Local Similarity 27.9%; Pred. No. 9.5e+02;
RESULT 1142
ID ABG25695 standard; protein; 705 AA.
DE Novel human diagnostic protein #55686.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 61.5; DB 4; Length 705;
Best Local Similarity 28.2%; Pred. No. 9.5e+02;
RESULT 1143
ID AAM93207 standard; protein; 739 AA.
DE Human polypeptide, SEQ ID NO: 2601.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INSTR.
Query Match 12.3%; Score 61.5; DB 4; Length 739;
Best Local Similarity 31.1%; Pred. No. 1e+03;
RESULT 1144
ID ADL30568 standard; protein; 739 AA.
DE Human protein encoded by a full length cDNA clone seqid 2601.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.3%; Score 61.5; DB 8; Length 739;
Best Local Similarity 31.1%; Pred. No. 1e+03;
RESULT 1145
ID AAB43831 standard; protein; 766 AA.
DE Human cancer associated protein sequence SEQ ID NO:1276.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 61.5; DB 3; Length 766;
Best Local Similarity 31.1%; Pred. No. 1.1e+03;
RESULT 1146
ID ABP41543 standard; protein; 766 AA.
DE Human ovarian antigen HPC1773, SEQ ID NO:2675.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 61.5; DB 5; Length 766;
Best Local Similarity 31.1%; Pred. No. 1.1e+03;
RESULT 1147
ID ABU38459 standard; protein; 820 AA.
DE Protein encoded by Prokaryotic essential gene #23986.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 820;
Best Local Similarity 37.3%; Pred. No. 1.2e+03;
RESULT 1148
ID ABM82561 standard; protein; 966 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:2810.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 966;
Best Local Similarity 27.3%; Pred. No. 1.4e+03;
RESULT 1149
ID ABB70304 standard; protein; 984 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37704.
PN WO200172042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 12.3%; Score 61.5; DB 4; Length 984;
Best Local Similarity 33.9%; Pred. No. 1.5e+03;
RESULT 1150
ID ABM82559 standard; protein; 1008 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2808.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 1008;
Best Local Similarity 27.3%; Pred. No. 1.5e+03;
RESULT 1151
ID AAB93169 standard; protein; 1014 AA.
DE Human protein sequence SEQ ID NO:12102.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INSTR.
Query Match 12.3%; Score 61.5; DB 4; Length 1014;
Best Local Similarity 27.3%; Pred. No. 1.5e+03;
RESULT 1152
ID ABM82563 standard; protein; 1041 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2812.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 1041;
Best Local Similarity 27.3%; Pred. No. 1.6e+03;
RESULT 1153
ID ADA05674 standard; protein; 1054 AA.
DE Human NOV6a protein SEQ ID NO:34.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 61.5; DB 6; Length 1054;
Best Local Similarity 27.3%; Pred. No. 1.6e+03;
RESULT 1154
ID ADN62839 standard; protein; 1054 AA.
DE Human NOV6a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUTJ/) JU J.
PA (LILU/) LI L.
PA (GUOK/) GUO X.
PA (PATY/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELER/) ELIERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRUSSEN B D.
PA (ANDE/) ANDERSON D W.
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PA (ZHON/) ZHONG M.
PD (CAT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1054;
RESULT 1155
ID ADM63232 standard; protein; 1054 AA.
DE Human NOV6a variant.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYN/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTERMAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CAT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1054;
RESULT 1156
ID ABW82562 standard; protein; 1076 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2811.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1076;
RESULT 1157
ID AAE14346 standard; protein; 1108 AA.
DE Human protease PRS-11 protein.
PD 2000183775-A2.

PD 08-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 5; Length 1108;
RESULT 1158
ID ABW82560 standard; protein; 1121 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2809.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1121;
RESULT 1159
ID ABW82558 standard; protein; 1128 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2807.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1128;
RESULT 1160
ID AD116339 standard; protein; 1145 AA.
DE Human protein modification and maintenance molecule (PMM) protein #24.
PD 04-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1145;
RESULT 1161
ID AD116340 standard; protein; 1165 AA.
DE Human protein modification and maintenance molecule (PMM) protein #25.
PD 04-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1165;
RESULT 1162
ID ABJ26652 standard; protein; 1236 AA.
DE Human protein modification + maintenance molecule protein SEQ ID No 6.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 6; Length 1236;
RESULT 1163
ID ABJ26649 standard; protein; 1256 AA.
DE Human protein modification + maintenance molecule protein SEQ ID No 3.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 6; Length 1256;
RESULT 1164
ID AAU68534 standard; protein; 1324 AA.
DE Human novel cytokine encoded by cDNA 790CIP2C_5 #1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 4; Length 1324;
RESULT 1165
ID AAU68535 standard; protein; 1346 AA.
DE Human novel cytokine encoded by cDNA 790CIP2C_6 #1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.3%; Score 61.5; DB 4; Length 1346;
RESULT 1166
ID ABG15667 standard; protein; 1444 AA.
DE Novel human diagnostic protein #15658.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 61.5; DB 4; Length 1444;
Best Local Similarity 28.8%; Pred. No. 2.4e+03;
RESULT 1167
ID AB035729 standard; protein; 2103 AA.
DE Protein encoded by Prokaryotic essential gene #21256.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 2103;
Best Local Similarity 27.5%; Pred. No. 4e+03;
RESULT 1168
ID AAB23751 standard; protein; 4881 AA.
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:5.
PN W0200050605-A1.
PD 31-AUG-2000.
PA (KITA) KITASATO INST.
Query Match 12.3%; Score 61.5; DB 3; Length 4881;
Best Local Similarity 28.3%; Pred. No. 1.2e+04;
RESULT 1169
ID AAG65266 standard; protein; 4881 AA.
DE Streptomyces avermitilis protein SEQ ID NO: 6.
PN W0200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.3%; Score 61.5; DB 4; Length 4881;
Best Local Similarity 28.3%; Pred. No. 1.2e+04;
RESULT 1170
ID ABO75855 standard; protein; 98 AA.
DE Pseudomonas aeruginosa polypeptide #8030.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 98;
Best Local Similarity 29.3%; Pred. No. 80;
RESULT 1171
ID ABP56643 standard; protein; 142 AA.
DE Chimpanzee C68 adenovirus hexon-associated protein PIX SEQ ID NO:8.
PN W02003000851-A2.
PD 03-JAN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.2%; Score 61; DB 6; Length 142;
Best Local Similarity 31.1%; Pred. No. 1.3e+02;
RESULT 1172
ID AB09748 standard; protein; 199 AA.
DE Mouse interleukin 11 (IL-11).
PN US2003008343-A1.
PD 09-JAN-2003.
PA (TIMA) TIMANS J C.
PA (PFLM) PFLANZ S K.
PA (KAST/) KASTELEIN R A.
PA (BAZA/) BAZAN J F.
Query Match 12.2%; Score 61; DB 6; Length 199;
Best Local Similarity 29.5%; Pred. No. 2e+02;
RESULT 1173
ID ABB09165 standard; protein; 212 AA.
DE Methylomonaas KHG/KDPG aldolase SEQ ID NO:10.
PN W0200202796-A2.
PD 14-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.2%; Score 61; DB 5; Length 212;
Best Local Similarity 29.5%; Pred. No. 2.2e+02;
RESULT 1174
ID AAE22300 standard; protein; 212 AA.
DE Methylomonaas 16a sp. KHG/KDPG aldolase enzyme.
PN W0200218617-A2.
PD 07-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.2%; Score 61; DB 5; Length 212;
Best Local Similarity 29.5%; Pred. No. 2.2e+02;
RESULT 1175
ID ABG61560 standard; protein; 212 AA.
DE High growth methanotrophic bacterial strain polypeptide #10.
PN W0200220728-A2.
PD 14-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.2%; Score 61; DB 5; Length 212;
Best Local Similarity 29.5%; Pred. No. 2.2e+02;
RESULT 1176
ID ABM67390 standard; protein; 233 AA.
DE Photorhabdus luminescens protein sequence #487.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.2%; Score 61; DB 6; Length 233;
Best Local Similarity 24.3%; Pred. No. 2.5e+02;
RESULT 1177
ID ABO78539 standard; protein; 236 AA.
DE Pseudomonas aeruginosa polypeptide #10714.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 236;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 1178
ID ADN26268 standard; protein; 256 AA.
DE Bacterial polypeptide #8921.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.2%; Score 61; DB 8; Length 256;
Best Local Similarity 25.0%; Pred. No. 2.8e+02;
RESULT 1179
ID ADJ98209 standard; protein; 269 AA.
DE Rice phytyl kinase protein.
PN W02004013312-A2.
PD 12-FEB-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 12.2%; Score 61; DB 8; Length 269;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 1180
ID ABO84568 standard; protein; 296 AA.
DE Mouse cancer-associated protein MPL6-049.1.
PN W02004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.2%; Score 61; DB 8; Length 296;
Best Local Similarity 25.9%; Pred. No. 3.4e+02;
RESULT 1181
ID ADJ98208 standard; protein; 314 AA.
DE Rice phytyl kinase protein.
PN W02004013312-A2.
PD 12-FEB-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 12.2%; Score 61; DB 8; Length 314;
Best Local Similarity 28.4%; Pred. No. 3.7e+02;
RESULT 1182
ID ABU39775 standard; protein; 329 AA.
DE Protein encoded by Prokaryotic essential gene #25302.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.2%; Score 61; DB 6; Length 329;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 1183
ID ABU36699 standard; protein; 343 AA.
DE Protein encoded by Prokaryotic essential gene #22226.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 12.2%; Score 61; DB 6; Length 343;
Best Local Similarity 23.9%; Pred. No. 4.2e+02;
RESULT 1184
ID ABO63783 standard; protein; 374 AA.
DE Klebsiella pneumoniae polypeptide seqid 10300.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 374;
Best Local Similarity 38.5%; Pred. No. 4.7e+02;
RESULT 1185
ID ADN23787 standard; protein; 390 AA.
DE Bacterial polypeptide #5440.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.2%; Score 61; DB 8; Length 390;
Best Local Similarity 30.6%; Pred. No. 4.9e+02;
RESULT 1186
ID ABR82131 standard; protein; 417 AA.
DE Bacterial P450 enzyme SEQ ID NO:26.
PN WO2003052050-A2.
PD 26-JUN-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 12.2%; Score 61; DB 6; Length 417;
Best Local Similarity 34.3%; Pred. No. 5.4e+02;
RESULT 1187
ID AAY81741 standard; protein; 419 AA.
DE Streptococcus pneumoniae protein sequence ID47.
PN WO200006738-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 12.2%; Score 61; DB 3; Length 419;
Best Local Similarity 29.4%; Pred. No. 5.4e+02;
RESULT 1188
ID ABUD01175 standard; protein; 419 AA.
DE S. pneumoniae type 4 strain protein from coding region #748.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.2%; Score 61; DB 6; Length 419;
Best Local Similarity 29.4%; Pred. No. 5.4e+02;
RESULT 1189
ID ADX46237 standard; protein; 419 AA.
DE Streptococcus pneumoniae protein, Seq ID No 2752.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 8; Length 419;
Best Local Similarity 29.4%; Pred. No. 5.4e+02;
RESULT 1190
ID AD95141 standard; protein; 425 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3776.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 8; Length 425;
Best Local Similarity 29.4%; Pred. No. 5.5e+02;
RESULT 1191
ID ABP66308 standard; protein; 430 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1052.
PN EP1227152-A1.
PD 31-JUN-2002.
PA (NEST-) SOC PROD NESTLE SA.
Query Match 12.2%; Score 61; DB 5; Length 430;
Best Local Similarity 29.4%; Pred. No. 5.6e+02;
RESULT 1192
ID AAM57832 standard; protein; 435 AA.

DE C1cm protein.
PN EP83909-A1.
PD 06-MAY-1998.
PA (UYGR-) RIJXSUNIV GRONINGEN.
Query Match 12.2%; Score 61; DB 2; Length 435;
Best Local Similarity 22.9%; Pred. No. 5.7e+02;
RESULT 1193
ID AAU44346 standard; protein; 455 AA.
DE Propionibacterium acnes immunogenic protein #5242.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.2%; Score 61; DB 4; Length 455;
Best Local Similarity 32.8%; Pred. No. 6.1e+02;
RESULT 1194
ID ABW40865 standard; protein; 455 AA.
DE Propionibacterium acnes immunogenic polypeptide #5541.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.2%; Score 61; DB 6; Length 455;
Best Local Similarity 32.8%; Pred. No. 6.1e+02;
RESULT 1195
ID ABB71149 standard; protein; 473 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40239.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 473;
Best Local Similarity 28.3%; Pred. No. 6.4e+02;
RESULT 1196
ID ABU22761 standard; protein; 474 AA.
DE Protein encoded by Prokaryotic essential gene #8288.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELITRA) ELITRA PHARM INC.
Query Match 12.2%; Score 61; DB 6; Length 474;
Best Local Similarity 32.3%; Pred. No. 6.4e+02;
RESULT 1197
ID ABP65910 standard; protein; 500 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:654.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST-) SOC PROD NESTLE SA.
Query Match 12.2%; Score 61; DB 5; Length 500;
Best Local Similarity 24.7%; Pred. No. 6.9e+02;
RESULT 1198
ID ADC13196 standard; protein; 505 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1478.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.2%; Score 61; DB 7; Length 505;
Best Local Similarity 31.6%; Pred. No. 7e+02;
RESULT 1199
ID ABG15005 standard; protein; 510 AA.
DE Novel human diagnostic protein #14996.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.2%; Score 61; DB 4; Length 510;
Best Local Similarity 31.6%; Pred. No. 7e+02;
RESULT 1200
ID ABU11797 standard; protein; 519 AA.
DE Human MDPY polypeptide SEQ ID 744.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.2%; Score 61; DB 6; Length 519;
Best Local Similarity 31.6%; Pred. No. 7.2e+02;
RESULT 1201
ID AAU07370 standard; protein; 524 AA.
DE G protein-coupled receptor.

PN WO200162924-A2.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 12.2%; Score 61; DB 4; Length 524;
Best Local Similarity 34.8%; Pred. No. 7.3e+02;
RESULT 1202
ID ABB06166 standard; protein; 528 AA.
DE Human liver with hepatitis related protein SEQ ID NO:12.
PN WO200200874-A1.
PD 03-JAN-2002.
PA (AJIN) AJINOMOTO CO INC.
Query Match 12.2%; Score 61; DB 5; Length 528;
Best Local Similarity 31.6%; Pred. No. 7.4e+02;
RESULT 1203
ID ABB67264 standard; protein; 545 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28584.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 545;
Best Local Similarity 32.0%; Pred. No. 7.7e+02;
RESULT 1204
ID ABB5578 standard; protein; 545 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2526.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 545;
Best Local Similarity 32.0%; Pred. No. 7.7e+02;
RESULT 1205
ID ADC08307 standard; protein; 549 AA.
DE Rice protein sequence Seq ID612 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 61; DB 7; Length 549;
Best Local Similarity 25.3%; Pred. No. 7.8e+02;
RESULT 1206
ID ADC07912 standard; protein; 549 AA.
DE Rice protein sequence Seq ID178 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 61; DB 7; Length 549;
Best Local Similarity 25.3%; Pred. No. 7.8e+02;
RESULT 1207
ID ADN63051 standard; protein; 568 AA.
DE Human NOV55D.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT) SMITHSON G.
PA (MILL) MILLET I.
PA (PEYM) PEYMAN J A.
PA (KEKU) KEKUDA R.
PA (JUJ) JU J.
PA (LILL) LI L.
PA (GUOX) GUO X.
PA (PATT) PATTURAJAN M.
PA (SPYT) SPYTEK K A.
PA (EDIN) EDINGER S R.
PA (ELLE) ELLERMAN K.
PA (MALY) MALYANKAR U M.
PA (ORTT) ORT T.
PA (GORM) GORMAN L.
PA (ZERR) ZERRHUSEN B D.
PA (ANDE) ANDERSON D W.
PA (ZHON) ZHONG M.
PA (CATI) CATERBERTON E.
PA (JIWW) JI W.
PA (MILL) MILLER C E.
PA (RAST) RASTELLI L.
PA (STON) STONE D J.
PA (PENA) PENA C E A.

PA (SHEN) SHENOY S G.
PA (SHIM) SHIMKETS R A.
PA (ROTH) ROTHENBERG M E.
PA (LEAC) LEACH M D.
PA (AGEE) AGEER M L.
PA (BERG) BERGHS C.
PA (DIFI) DIPPEO V A.
PA (EISE) EISEN A.
PA (GANG) GANGOLI E A.
PA (RIEG) RIEGER D K.
PA (SPAD) SPADERNA S K.
Query Match 12.2%; Score 61; DB 8; Length 568;
Best Local Similarity 20.0%; Pred. No. 8.1e+02;
RESULT 1208
ID ADO42971 standard; protein; 579 AA.
DE Murine fatty acid amide hydrolase (FAAH), SEQ ID NO:4.
PN WO2004037371-A2.
PD 06-MAY-2004.
PA (JANC) JANSSEN PHARM NV.
Query Match 12.2%; Score 61; DB 8; Length 579;
Best Local Similarity 29.2%; Pred. No. 8.3e+02;
RESULT 1209
ID AAW57782 standard; protein; 581 AA.
DE Mouse fatty acid amide hydrolase.
PN WO9820119-A1.
PD 14-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 12.2%; Score 61; DB 2; Length 581;
Best Local Similarity 29.2%; Pred. No. 8.4e+02;
RESULT 1210
ID ABU38916 standard; protein; 582 AA.
DE Protein encoded by Prokaryotic essential gene #24443.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT) ELITRA PHARM INC.
Query Match 12.2%; Score 61; DB 6; Length 582;
Best Local Similarity 26.8%; Pred. No. 8.4e+02;
RESULT 1211
ID ABO70115 standard; protein; 588 AA.
DE Pseudomonas aeruginosa polypeptide #2290.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 588;
Best Local Similarity 26.8%; Pred. No. 8.5e+02;
RESULT 1212
ID ADP31467 standard; protein; 618 AA.
DE Human secreted protein SEQ ID #2234.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE) FIVE PRIME THERAPEUTICS INC.
Query Match 12.2%; Score 61; DB 8; Length 618;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
RESULT 1213
ID ADP31466 standard; protein; 618 AA.
DE Human secreted protein SEQ ID #2233.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE) FIVE PRIME THERAPEUTICS INC.
Query Match 12.2%; Score 61; DB 8; Length 618;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
RESULT 1214
ID ADS30153 standard; protein; 620 AA.
DE Bacterial polypeptide #19186.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SIAT) SIATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 12.2%; Score 61; DB 8; Length 620;
Best Local Similarity 27.1%; Pred. No. 9.1e+02;

RESULT 1215
ID ABB66879 standard; protein; 637 AA.
DE Drosophila melanogaster polypeptide SHQ ID NO 27429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 637;
Best Local Similarity 32.0%; Pred. No. 9.4e+02;
RESULT 1216
ID ADJ98211 standard; protein; 657 AA.
DE Rice phytoel kinase protein.
PN WO2004013312-A2.
PD 12-FEB-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 12.2%; Score 61; DB 8; Length 657;
Best Local Similarity 28.4%; Pred. No. 9.8e+02;
RESULT 1217
ID AAY37620 standard; protein; 658 AA.
DE Protein involved in transcription, translation and/or maturation.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GSEST) GENSET.
Query Match 12.2%; Score 61; DB 2; Length 658;
Best Local Similarity 27.9%; Pred. No. 9.8e+02;
RESULT 1218
ID ABB61294 standard; protein; 693 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10674.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 693;
Best Local Similarity 39.0%; Pred. No. 1.1e+03;
RESULT 1219
ID ABO69796 standard; protein; 707 AA.
DE Pseudomonas aeruginosa polypeptide #1971.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 707;
Best Local Similarity 35.3%; Pred. No. 1.1e+03;
RESULT 1220
ID ABU19429 standard; protein; 769 AA.
DE Protein encoded by prokaryotic essential gene #4956.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.2%; Score 61; DB 6; Length 769;
Best Local Similarity 31.8%; Pred. No. 1.2e+03;
RESULT 1221
ID AAR45001 standard; protein; 802 AA.
DE Cellulose synthase operon, gene B product.
PN US2568274-A.
PD 07-DEC-1993.
PA (CETU) CETUS CORP.
Query Match 12.2%; Score 61; DB 2; Length 802;
Best Local Similarity 25.8%; Pred. No. 1.3e+03;
RESULT 1222
ID ADJ98210 standard; protein; 803 AA.
DE Rice phytoel kinase protein.
PN WO2004013312-A2.
PD 12-FEB-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 12.2%; Score 61; DB 8; Length 803;
Best Local Similarity 28.4%; Pred. No. 1.3e+03;
RESULT 1223
ID ADS42575 standard; protein; 873 AA.
DE Bacterial polypeptide #21005.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PD (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.
Query Match 12.2%; Score 61; DB 8; Length 873;
Best Local Similarity 27.5%; Pred. No. 1.4e+03;
RESULT 1224
ID AAB6456 standard; protein; 920 AA.
DE Protein encoded by Mycobacterium tuberculosis mmpL7 (RV2942) gene.
PN WO200102555-A1.
PD 11-JAN-2001.
PA (INSP) INST PASTEUR.
Query Match 12.2%; Score 61; DB 4; Length 920;
Best Local Similarity 28.0%; Pred. No. 1.5e+03;
RESULT 1225
ID ABR55195 standard; protein; 920 AA.
DE Nucleotide sequence of gene down-regulated during nutrient starvation.
PN WO2003035681-A2.
PD 01-MAY-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 12.2%; Score 61; DB 6; Length 920;
Best Local Similarity 28.0%; Pred. No. 1.5e+03;
RESULT 1226
ID ABO68019 standard; protein; 927 AA.
DE Pseudomonas aeruginosa polypeptide #194.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.2%; Score 61; DB 7; Length 927;
Best Local Similarity 25.7%; Pred. No. 1.5e+03;
RESULT 1227
ID ADJ80167 standard; protein; 1006 AA.
DE Novel human nucleic acid-associated protein #43.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.2%; Score 61; DB 7; Length 1006;
Best Local Similarity 28.7%; Pred. No. 1.7e+03;
RESULT 1228
ID ABB64908 standard; protein; 1044 AA.
DE Human protein SEQ ID 568.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYGR-) HYSEQ INC.
Query Match 12.2%; Score 61; DB 5; Length 1044;
Best Local Similarity 28.7%; Pred. No. 1.8e+03;
RESULT 1229
ID ABB61832 standard; protein; 1086 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12288.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 61; DB 4; Length 1086;
Best Local Similarity 33.9%; Pred. No. 1.9e+03;
RESULT 1230
ID ADS96730 standard; protein; 1086 AA.
DE Drosophila melanogaster protein, SEQ ID 351.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 61; DB 8; Length 1086;
Best Local Similarity 33.9%; Pred. No. 1.9e+03;
RESULT 1231
ID ADB64795 standard; protein; 1166 AA.
DE Human protein encoded by clone NTONG20053630.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.2%; Score 61; DB 7; Length 1166;
Best Local Similarity 28.7%; Pred. No. 2.1e+03;
RESULT 1232
ID ADG42630 standard; protein; 1531 AA.
DE Mouse SLIT1.
PN US2003204052-A1.
PD 30-OCT-2003.

PA (HERR/) HERRMANN J L.
PA (RAST/) RASTFELI L.
PA (SHIM/) SHIMKETS R. A.
Query Match 12.2%; Score 61; DB 7; Length 1531;
Best Local Similarity 27.7%; Pred. No. 3e+03;
RESULT 1233
ID AAM18305 standard; protein; 1565 AA.
DE Photorhabdus luminescens insect toxin Tccb.
PN MO9717432-A1.
PD 15-MAY-1997.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 12.2%; Score 61; DB 2; Length 1565;
Best Local Similarity 35.1%; Pred. No. 3.1e+03;
RESULT 1234
ID ABG97432 standard; protein; 1977 AA.
DE S. carzinostaticus FKSE protein.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPRIA BIOSCIENCES INC.
Query Match 12.2%; Score 61; DB 5; Length 1977;
Best Local Similarity 30.2%; Pred. No. 4.2e+03;
RESULT 1235
ID ADM45916 standard; protein; 3696 AA.
DE S. mycarofaciens mddecamycin polyketide synthetase ORF3 protein.
PN JP2004049100-A.
PD 19-FEB-2004.
PA (MEIT) MEITI SEIKA KAISHA LTD.
Query Match 12.2%; Score 61; DB 8; Length 3696;
Best Local Similarity 27.6%; Pred. No. 9.5e+03;
RESULT 1236
ID ADP31425 standard; protein; 8976 AA.
DE Human secreted protein SEQ ID #2192.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.2%; Score 61; DB 8; Length 8976;
Best Local Similarity 38.5%; Pred. No. 3e+04;
RESULT 1237
ID ADP31494 standard; protein; 9195 AA.
DE Human secreted protein SEQ ID #2261.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.2%; Score 61; DB 8; Length 9195;
Best Local Similarity 38.5%; Pred. No. 3.1e+04;
RESULT 1238
ID ABB62457 standard; protein; 138 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14163.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 60.5; DB 4; Length 138;
Best Local Similarity 23.3%; Pred. No. 1.4e+02;
RESULT 1239
ID AAG50109 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63463.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 144;
Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 1240
ID AAG07169 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4219.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 144;
Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 1241
ID AAG05467 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1883.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 144;

Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 1242
ID AAG48112 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60724.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 144;
Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 1243
ID ABP99217 standard; protein; 159 AA.
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 21.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPRIA BIOSCIENCES INC.
Query Match 12.1%; Score 60.5; DB 6; Length 159;
Best Local Similarity 25.3%; Pred. No. 1.7e+02;
RESULT 1244
ID ABU15772 standard; protein; 192 AA.
DE Protein encoded by Prokaryotic essential gene #1299.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 192;
Best Local Similarity 29.3%; Pred. No. 2.2e+02;
RESULT 1245
ID AAG07168 standard; protein; 196 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4218.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 196;
Best Local Similarity 28.0%; Pred. No. 2.3e+02;
RESULT 1246
ID AAG05466 standard; protein; 196 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1882.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 196;
Best Local Similarity 28.0%; Pred. No. 2.3e+02;
RESULT 1247
ID AAG50108 standard; protein; 196 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63462.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 196;
Best Local Similarity 28.0%; Pred. No. 2.3e+02;
RESULT 1248
ID AAG48111 standard; protein; 196 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60723.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 196;
Best Local Similarity 28.0%; Pred. No. 2.3e+02;
RESULT 1249
ID AAG50107 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63461.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 209;
Best Local Similarity 28.0%; Pred. No. 2.5e+02;
RESULT 1250
ID AAG05465 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1881.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 209;
Best Local Similarity 28.0%; Pred. No. 2.5e+02;
RESULT 1251
ID AAG07167 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4217.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 60.5; DB 3; Length 209;
Best Local Similarity 28.0%; Pred. No. 2.5e+02;

RESULT 1252
ID AAG48110 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60722.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 3; Length 209;
RESULT 1253
ID ABU44901 standard; protein; 249 AA.
DE Protein encoded by Prokaryotic essential gene #30428.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 6; Length 249;
RESULT 1254
ID ABB54446 standard; protein; 297 AA.
DE Lactococcus lactis protein ylec.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 5; Length 297;
RESULT 1255
ID ABU24698 standard; protein; 301 AA.
DE Protein encoded by Prokaryotic essential gene #10225.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 6; Length 301;
RESULT 1256
ID AAB76785 standard; protein; 304 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO:552.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 304;
RESULT 1257
ID ADR08655 standard; protein; 304 AA.
DE Human protein useful for treating neurological disease Seq 2161.
PN EPI44713-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 304;
RESULT 1258
ID AAG92285 standard; protein; 309 AA.
DE C glutamicum protein fragment SEQ ID NO: 6039.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 309;
RESULT 1259
ID ABU47526 standard; protein; 312 AA.
DE Protein encoded by Prokaryotic essential gene #33053.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 6; Length 312;
RESULT 1260
ID ADR43268 standard; protein; 325 AA.
DE IPT-like structural protein #337.
PN WO200407442-A2.
PD 02-SEP-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 325;
RESULT 1261
ID ABU26210 standard; protein; 340 AA.
DE Protein encoded by Prokaryotic essential gene #11737.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 6; Length 340;
RESULT 1262
ID AAW72102 standard; protein; 341 AA.
DE HSV-2 strain SBS Contig ID 10 ORF#8 protein.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMRK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 2; Length 341;
RESULT 1263
ID AAG52435 standard; protein; 341 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66652.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 3; Length 341;
RESULT 1264
ID ADO29667 standard; protein; 341 AA.
DE Mouse GPCR TRXA2R, SEQ ID NO:769.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 341;
RESULT 1265
ID AAW72015 standard; protein; 345 AA.
DE HSV-2 strain SBS Contig ID 102 ORF#1 protein.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMRK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 2; Length 345;
RESULT 1266
ID ABP26052 standard; protein; 352 AA.
DE Streptococcus polypeptide SEQ ID NO 1280.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 12.3%; Score 60.5; DB 5; Length 352;
RESULT 1267
ID ABM85262 standard; protein; 354 AA.
DE Mouse protein sequence MCP7634.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 7; Length 354;
RESULT 1268
ID ADR67011 standard; protein; 354 AA.
DE Mouse cancer associated protein sequence SEQ ID NO:57.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 354;
RESULT 1269
ID ADP30505 standard; protein; 357 AA.
DE Human secreted protein SEQ ID #1272.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 357;
RESULT 1270
ID ABU47532 standard; protein; 367 AA.
DE Protein encoded by Prokaryotic essential gene #33059.

PN W0200277183-A2.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 367;
Best Local Similarity 24.5%; Pred. No. 5.2e+02;
RESULT 1271
ID ABU46966 standard; protein; 367 AA.
DE Protein encoded by Prokaryotic essential gene #32493.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 367;
Best Local Similarity 24.5%; Pred. No. 5.2e+02;
RESULT 1272
ID AAG64284 standard; protein; 382 AA.
DE Rice gibberellin 2beta-hydroxylase.
PN W0200148215-A1.
PD 05-JUL-2001.
PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
PA (RIKE) RIKEN KK.
Query Match 12.1%; Score 60.5; DB 4; Length 382;
Best Local Similarity 27.2%; Pred. No. 5.5e+02;
RESULT 1273
ID ADK00083 standard; protein; 382 AA.
DE Rice gibberellin 2-oxidase, OSG2ox1.
PN US2004060080-A1.
PD 25-MAR-2004.
PA (NAG-) NAT INST AGROBIOLOGICAL SCI.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 12.1%; Score 60.5; DB 8; Length 382;
Best Local Similarity 27.2%; Pred. No. 5.5e+02;
RESULT 1274
ID AAM41928 standard; protein; 383 AA.
DE Human polypeptide SEQ ID NO 6859.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 60.5; DB 4; Length 383;
Best Local Similarity 30.6%; Pred. No. 5.5e+02;
RESULT 1275
ID ABO63274 standard; protein; 391 AA.
DE Klebsiella pneumoniae polypeptide seqid 9791.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.1%; Score 60.5; DB 7; Length 391;
Best Local Similarity 30.4%; Pred. No. 5.7e+02;
RESULT 1276
ID ABU36811 standard; protein; 401 AA.
DE Protein encoded by Prokaryotic essential gene #22338.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 401;
Best Local Similarity 35.4%; Pred. No. 5.8e+02;
RESULT 1277
ID ABR42482 standard; protein; 402 AA.
DE Coumermycin A1 biosynthetic glycosyltransferase.
PN W02003014352-A2.
PD 20-FEB-2003.
PA (UYTU-) UNIV TUEBINGEN.
Query Match 12.1%; Score 60.5; DB 6; Length 402;
Best Local Similarity 26.8%; Pred. No. 5.9e+02;
RESULT 1278
ID ABU34528 standard; protein; 412 AA.
DE Protein encoded by Prokaryotic essential gene #20055.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 412;
Best Local Similarity 35.4%; Pred. No. 6.1e+02;
RESULT 1279
ID AAM72232 standard; protein; 414 AA.

DE HSV-2 strain SBS Contig ID 15 ORF#46b protein.
PN W09820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.1%; Score 60.5; DB 2; Length 414;
Best Local Similarity 31.8%; Pred. No. 6.1e+02;
RESULT 1280
ID ADQ96058 standard; protein; 415 AA.
DE T cell activation associated protein #118.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 12.1%; Score 60.5; DB 8; Length 415;
Best Local Similarity 33.6%; Pred. No. 6.1e+02;
RESULT 1281
ID ADQ96060 standard; protein; 415 AA.
DE T cell activation associated protein #119.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 12.1%; Score 60.5; DB 8; Length 415;
Best Local Similarity 33.6%; Pred. No. 6.1e+02;
RESULT 1282
ID ABO76672 standard; protein; 420 AA.
DE Pseudomonas aeruginosa polypeptide #8847.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.1%; Score 60.5; DB 7; Length 420;
Best Local Similarity 39.0%; Pred. No. 6.2e+02;
RESULT 1283
ID ABG32423 standard; protein; 448 AA.
DE Human secreted protein #1.
PN W0200264626-A2.
PD 22-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 60.5; DB 5; Length 448;
Best Local Similarity 31.7%; Pred. No. 6.8e+02;
RESULT 1284
ID ABU40066 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #25593.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.1%; Score 60.5; DB 6; Length 458;
Best Local Similarity 29.0%; Pred. No. 7e+02;
RESULT 1285
ID AAM72231 standard; protein; 462 AA.
DE HSV-2 strain SBS Contig ID 15 ORF#46a protein.
PN W09820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.1%; Score 60.5; DB 2; Length 462;
Best Local Similarity 31.8%; Pred. No. 7e+02;
RESULT 1286
ID ADN21440 standard; protein; 470 AA.
DE Bacterial polypeptide #4093.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.1%; Score 60.5; DB 8; Length 470;
Best Local Similarity 32.0%; Pred. No. 7.2e+02;
RESULT 1287
ID AAM40142 standard; protein; 476 AA.
DE Human polypeptide SEQ ID NO 3287.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 60.5; DB 4; Length 476;

Best Local Similarity 30.6%; Pred. No. 7.3e+02;
RESULT 1288
ID ADQ96066 standard; protein; 499 AA.
DE T cell activation associated protein #122.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 499;
RESULT 1289
ID ADQ96064 standard; protein; 499 AA.
DE T cell activation associated protein #121.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 499;
RESULT 1290
ID ADJ48347 standard; protein; 515 AA.
DE Maize cjl-associated gene protein #6.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 515;
RESULT 1291
ID AAM85864 standard; protein; 535 AA.
DE Mouse protein sequence mcp8121.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 7; Length 535;
RESULT 1292
ID AAB67476 standard; protein; 538 AA.
DE Amino acid sequence of a Mumps virus protein.
PN WO200109309-A2.
PD 08-FEB-2001.
PA (AMMP-) AMERICAN HOME PROD CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 538;
RESULT 1293
ID ABM70178 standard; protein; 542 AA.
DE Photorhabdus luminescens protein sequence #3275.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS-) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 6; Length 542;
RESULT 1294
ID ADR95242 standard; protein; 574 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3877.
PN US8600744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 574;
RESULT 1295
ID ABP28684 standard; protein; 577 AA.
DE Streptococcus polypeptide SEQ ID NO 6544.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 5; Length 577;
RESULT 1296
ID AAB93779 standard; protein; 595 AA.

DE Human protein sequence SEQ ID NO:13509.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 595;
RESULT 1297
ID AAG91443 standard; protein; 600 AA.
DE C glutamicum protein fragment SEQ ID NO: 5197.
PN EPI08790-A2.
PD 20-JUN-2001.
PA (KYOW-) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 600;
RESULT 1298
ID ADH87898 standard; protein; 601 AA.
DE Enterococcus faecalis polypeptide #2378.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 7; Length 601;
RESULT 1299
ID ABG04210 standard; protein; 617 AA.
DE Novel human diagnostic protein #4201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 4; Length 617;
RESULT 1300
ID AAY01402 standard; protein; 621 AA.
DE Secreted protein encoded by gene 20 clone HGCA662.
PN WO9903990-A1.
PD 28-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 2; Length 621;
RESULT 1301
ID ABO23308 standard; protein; 621 AA.
DE Human secreted protein #20.
PN US200305045-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (YOIN/) YOUNG P E.
PA (GREB/) GREENE J M.
PA (NIJU/) NI J.
PA (FENG/) FENG P.
PA (FLOR/) FLORENCE K A.
PA (HUJU/) HU J.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (DUAN/) DUAN R D.
PA (JANA/) JANAT F.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 7; Length 621;
RESULT 1302
ID ADQ96062 standard; protein; 621 AA.
DE T cell activation associated protein #120.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 8; Length 621;
RESULT 1303
ID AAP60616 standard; protein; 774 AA.
DE Cephalosporin C acylase.
PN JP61152286-A.
PD 10-JUL-1986.
PA (ASAH-) ASAH CHEM IND CO LTD.
Query Match
Best Local Similarity 12.1%; Score 60.5; DB 1; Length 774;

Best Local Similarity 32.1%; Pred. No. 1.4e+03;
RESULT 1304
ID ADP30506 standard; protein; 774 AA.
DE Human secreted protein SEQ ID #1273.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.1%; Score 60.5; DB 8; Length 774;
Best Local Similarity 36.4%; Pred. No. 1.4e+03;
RESULT 1305
ID ABB54868 standard; protein; 867 AA.
DE Lactococcus lactis protein cIjB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 12.1%; Score 60.5; DB 5; Length 867;
Best Local Similarity 23.9%; Pred. No. 1.6e+03;
RESULT 1306
ID ADS29415 standard; protein; 867 AA.
DE Bacterial polypeptide #18448.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.1%; Score 60.5; DB 8; Length 867;
Best Local Similarity 23.9%; Pred. No. 1.6e+03;
RESULT 1307
ID ABB62035 standard; protein; 950 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12897.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 60.5; DB 4; Length 950;
Best Local Similarity 32.9%; Pred. No. 1.8e+03;
RESULT 1308
ID ABG07645 standard; protein; 1114 AA.
DE Novel human diagnostic protein #7636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 60.5; DB 4; Length 1114;
Best Local Similarity 26.1%; Pred. No. 2.2e+03;
RESULT 1309
ID ABO83693 standard; protein; 1118 AA.
DE Pseudomonas aeruginosa polypeptide #15868.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.1%; Score 60.5; DB 7; Length 1118;
Best Local Similarity 37.3%; Pred. No. 2.3e+03;
RESULT 1310
ID ADJ70257 standard; protein; 1191 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID2063.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.1%; Score 60.5; DB 7; Length 1191;
Best Local Similarity 30.6%; Pred. No. 2.4e+03;
RESULT 1311
ID ADD67541 standard; protein; 1606 AA.
DE Human ly1484p protein SEQ ID NO:18.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.1%; Score 60.5; DB 7; Length 1606;
Best Local Similarity 25.4%; Pred. No. 3.6e+03;
RESULT 1312
ID ADL05773 standard; protein; 2142 AA.
DE M. catarrhalis protein #1539.

PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.1%; Score 60.5; DB 8; Length 2142;
Best Local Similarity 27.2%; Pred. No. 5.3e+03;
RESULT 1313
ID AAU30691 standard; protein; 107 AA.
DE Novel human secreted protein #1182.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 107;
Best Local Similarity 28.2%; Pred. No. 1.2e+02;
RESULT 1314
ID AAW72908 standard; protein; 130 AA.
DE Mycobacterium tuberculosis antigen CFP16.
PN WO9844119-A1.
PD 08-OCT-1998.
PA (STAT-) STATENS SERUM INST.
Query Match 12.0%; Score 60; DB 2; Length 130;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;
RESULT 1315
ID AAY21925 standard; protein; 130 AA.
DE Amino acid sequence of antigen CFP16.
PN WO9924577-A1.
PD 20-MAY-1999.
PA (STAT-) STATENS SERUM INST.
Query Match 12.0%; Score 60; DB 2; Length 130;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;
RESULT 1316
ID AAM50746 standard; protein; 130 AA.
DE Mycobacterium tuberculosis immunodominant Mtb protein RplL.
PN WO200204018-A2.
PD 17-JAN-2002.
PA (COLS) UNIV COLORADO STATE RES FOUND.
Query Match 12.0%; Score 60; DB 5; Length 130;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;
RESULT 1317
ID ABU34454 standard; protein; 130 AA.
DE Protein encoded by Prokaryotic essential gene #19981.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 130;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;
RESULT 1318
ID ABU36489 standard; protein; 130 AA.
DE Protein encoded by Prokaryotic essential gene #22016.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 130;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;
RESULT 1319
ID ADE63753 standard; protein; 157 AA.
DE Rat Protein CAA42203, SEQ ID NO 9697.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.0%; Score 60; DB 7; Length 157;
Best Local Similarity 36.2%; Pred. No. 1.9e+02;
RESULT 1320
ID ADC88215 standard; protein; 179 AA.
DE Ribosomal protein similar to FCWP1 #431.
PN US6573361-B1.
PD 03-JUN-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 12.0%; Score 60; DB 7; Length 179;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
RESULT 1321
ID ABO00479 standard; protein; 196 AA.
DE Novel human polypeptide #66.

PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 196;
RESULT 1322
ID ABU20750 standard; protein; 206 AA.
DE Protein encoded by Prokaryotic essential gene #6277.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 206;
RESULT 1323
ID ABO83684 standard; protein; 208 AA.
DE Pseudomonas aeruginosa polypeptide #15859.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 208;
RESULT 1324
ID ADS23376 standard; protein; 209 AA.
DE Bacterial polypeptide #12409.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 209;
RESULT 1325
ID ABP29761 standard; protein; 230 AA.
DE Streptococcus polypeptide SEQ ID NO 8698.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 230;
RESULT 1326
ID ABG96327 standard; protein; 232 AA.
DE Human ovarian cancer marker M444.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 232;
RESULT 1327
ID ABP26904 standard; protein; 238 AA.
DE Streptococcus polypeptide SEQ ID NO 2984.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 238;
RESULT 1328
ID ABU22030 standard; protein; 240 AA.
DE Protein encoded by Prokaryotic essential gene #7557.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 240;
RESULT 1329
ID ABB09051 standard; protein; 263 AA.
DE Thermus caldophilus GK24 cosmid clone 3 related protein SEQ ID NO:3.
PN KR2001019888-A.
PD 15-MAR-2001.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 263;
RESULT 1330
ID ABO67879 standard; protein; 264 AA.
DE Pseudomonas aeruginosa polypeptide #54.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 264;
RESULT 1331
ID ADN26129 standard; protein; 270 AA.
DE Bacterial polypeptide #8782.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 270;
RESULT 1332
ID AAU91157 standard; protein; 273 AA.
DE Treponema pallidum pantothenate Kinase Coax.
PN WO200216601-A2.
PD 28-FEB-2002.
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 273;
RESULT 1333
ID ABB16116 standard; peptide; 307 AA.
DE Peptide #3622 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;
RESULT 1334
ID AAM29607 standard; protein; 307 AA.
DE Peptide #3644 encoded by probe for measuring placental gene expression.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;
RESULT 1335
ID ABB10928 standard; peptide; 307 AA.
DE Peptide #3579 encoded by breast cell single exon nucleic acid probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;
RESULT 1336
ID ABB21504 standard; protein; 307 AA.
DE Protein #3503 encoded by probe for measuring heart cell gene expression.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;
RESULT 1337
ID AAM69287 standard; protein; 307 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29593.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;
RESULT 1338
ID AAM56899 standard; protein; 307 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29004.

PN WO200157275-A2.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.0%; Score 60; DB 4; Length 307;
Best Local Similarity 43.6%; Pred. No. 4.7e+02;
RESULT 1339
ID ABG39901 standard; peptide; 307 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28566.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.0%; Score 60; DB 5; Length 307;
Best Local Similarity 43.6%; Pred. No. 4.7e+02;
RESULT 1340
ID AAM39798 standard; protein; 308 AA.
DE Human polypeptide SEQ ID NO 2943.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1341
ID AAE25381 standard; protein; 308 AA.
DE Human NZMS-5 protein.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 60; DB 5; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1342
ID AAE21813 standard; protein; 308 AA.
DE Human 46873 asparaginase.
PN US2002038014-A1.
PD 28-MAR-2002.
PA (MEYE/) MEYERS R. A.
Query Match 12.0%; Score 60; DB 5; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1343
ID AAE37617 standard; protein; 308 AA.
DE Human 25943 (glycosylasparaginase) protein.
PN WO2003038113-A2.
PD 08-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1344
ID AAE29747 standard; protein; 308 AA.
DE Novel human asparaginase (NHA) protein.
PN WO200277219-A1.
PD 03-OCT-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.0%; Score 60; DB 6; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1345
ID ADB64580 standard; protein; 308 AA.
DE Human protein encoded by clone KIDN20083620.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.0%; Score 60; DB 7; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1346
ID ADB64015 standard; protein; 308 AA.
DE Human protein encoded by clone BRAMY20125360.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.0%; Score 60; DB 7; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1347
ID ADC26179 standard; protein; 308 AA.

DE Human NOV2a protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1348
ID ADC26185 standard; protein; 308 AA.
DE Human NOV2d protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1349
ID ADC26183 standard; protein; 308 AA.
DE Human NOV2c protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 308;
Best Local Similarity 28.0%; Pred. No. 4.7e+02;
RESULT 1350
ID ADC26189 standard; protein; 312 AA.
DE Human NOV2f protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 312;
Best Local Similarity 28.0%; Pred. No. 4.8e+02;
RESULT 1351
ID ADC26191 standard; protein; 312 AA.
DE Human NOV2g protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 312;
Best Local Similarity 28.0%; Pred. No. 4.8e+02;
RESULT 1352
ID ADO30431 standard; protein; 313 AA.
DE Mouse GPCR OR212, SEQ ID NO:1534.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 12.0%; Score 60; DB 8; Length 313;
Best Local Similarity 34.3%; Pred. No. 4.8e+02;
RESULT 1353
ID ADC26187 standard; protein; 314 AA.
DE Human NOV2e protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 314;
Best Local Similarity 28.0%; Pred. No. 4.8e+02;
RESULT 1354
ID AUB38294 standard; protein; 321 AA.
DE Salmonella typhi cellular proliferation protein #185.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 4; Length 321;
Best Local Similarity 26.1%; Pred. No. 5e+02;
RESULT 1355
ID AAG39429 standard; protein; 321 AA.
DE Escherichia coli protein sequence SEQ ID NO:477.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 4; Length 321;
Best Local Similarity 27.0%; Pred. No. 5e+02;
RESULT 1356
ID ABP41427 standard; protein; 321 AA.
DE Human ovarian antigen HRP5H76, SEQ ID NO:2559.

PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 321;
RESULT 1357
ID ABU44809 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #30336.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;
RESULT 1358
ID ABU48212 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #33739.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;
RESULT 1359
ID ABU4841 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #368.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;
RESULT 1360
ID ABU47031 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #32558.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;
RESULT 1361
ID ABO72294 standard; protein; 331 AA.
DE Pseudomonas aeruginosa polypeptide #4469.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 331;
RESULT 1362
ID ABB52481 standard; protein; 336 AA.
DE Escherichia coli polypeptide SEQ ID NO 305.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM NAT SANTE & RECH MEDICALE.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 336;
RESULT 1363
ID ABO63632 standard; protein; 337 AA.
DE Klebsiella pneumoniae polypeptide seqid 10149.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 337;
RESULT 1364
ID ABG28657 standard; protein; 342 AA.
DE Novel human diagnostic protein #28648.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 342;
RESULT 1365
ID AAY38901 standard; protein; 343 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF125.
PN WO9924578-A2.

PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 12.0%; Score 60; DB 2; Length 343;
RESULT 1366
ID AAM41584 standard; protein; 346 AA.
DE Human polypeptide SEQ ID NO 6515.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 346;
RESULT 1367
ID AAM98317 standard; protein; 350 AA.
DE H. pylori GHP0 1024 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 2; Length 350;
RESULT 1368
ID ABG24784 standard; protein; 369 AA.
DE Novel human diagnostic protein #24775.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 369;
RESULT 1369
ID ABR52878 standard; protein; 371 AA.
DE Protein sequence #SEQ ID 621.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 371;
RESULT 1370
ID ADK62082 standard; protein; 371 AA.
DE Disease treating protein complex-derived protein #167.
PN EPI38608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 371;
RESULT 1371
ID ADS43667 standard; protein; 371 AA.
DE Bacterial polypeptide #22097.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 371;
RESULT 1372
ID ABU49108 standard; protein; 372 AA.
DE Protein encoded by Prokaryotic essential gene #34635.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 372;
RESULT 1373
ID ADA33213 standard; protein; 381 AA.
DE Acinetobacter baumannii protein #374.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 381;
PD 26.8%; Pred. No. 6.2e+02;

RESULT 1374
ID ABP77627 standard; protein; 392 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 1784.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 12.0%; Score 60; DB 6; Length 392;
Best Local Similarity 29.6%; Pred. No. 6.5e+02;
RESULT 1375
ID AAM51351 standard; protein; 402 AA.
DE P. velutina lectin protein sequence.
PN W09816825-A1.
PD 23-APR-1998.
PA (SEGG) SEIRGAKU CORP.
Query Match 12.0%; Score 60; DB 2; Length 402;
Best Local Similarity 28.2%; Pred. No. 6.7e+02;
RESULT 1376
ID ADP31390 standard; protein; 402 AA.
DE Human secreted protein SEQ ID #2157.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.0%; Score 60; DB 8; Length 402;
Best Local Similarity 36.0%; Pred. No. 6.7e+02;
RESULT 1377
ID AAY38902 standard; protein; 408 AA.
DE Neisseria gonorrhoeae antigen encoded by ORF125.
PN W09924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 12.0%; Score 60; DB 2; Length 408;
Best Local Similarity 32.6%; Pred. No. 6.8e+02;
RESULT 1378
ID ADC26181 standard; protein; 426 AA.
DE Human NOV2b protein.
PN W02003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 7; Length 426;
Best Local Similarity 28.0%; Pred. No. 7.2e+02;
RESULT 1379
ID ABO72701 standard; protein; 435 AA.
DE Pseudomonas aeruginosa polypeptide #4876.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 60; DB 7; Length 435;
Best Local Similarity 31.1%; Pred. No. 7.4e+02;
RESULT 1380
ID ABB06896 standard; protein; 438 AA.
DE Micromonospora carbonacea evernimicin locus protein ORF 16.
PN W020015180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match 12.0%; Score 60; DB 4; Length 438;
Best Local Similarity 25.6%; Pred. No. 7.5e+02;
RESULT 1381
ID ABP99230 standard; protein; 438 AA.
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 47.
PN W0200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 6; Length 438;
Best Local Similarity 25.6%; Pred. No. 7.5e+02;
RESULT 1382
ID ABU39628 standard; protein; 450 AA.
DE Protein encoded by Prokaryotic essential gene #25155.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 450;
Best Local Similarity 30.7%; Pred. No. 7.7e+02;

RESULT 1383
ID ABU22956 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #8483.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 453;
Best Local Similarity 26.8%; Pred. No. 7.8e+02;
RESULT 1384
ID AAY75758 standard; protein; 466 AA.
DE Neisseria meningitidis ORF 989 protein sequence SEQ ID NO:2988.
PN W09957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 12.0%; Score 60; DB 3; Length 466;
Best Local Similarity 26.2%; Pred. No. 8.1e+02;
RESULT 1385
ID ABO72512 standard; protein; 467 AA.
DE Pseudomonas aeruginosa polypeptide #4687.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 60; DB 7; Length 467;
Best Local Similarity 28.6%; Pred. No. 8.1e+02;
RESULT 1386
ID ADS23989 standard; protein; 479 AA.
DE Bacterial polypeptide #13022.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 479;
Best Local Similarity 26.7%; Pred. No. 8.4e+02;
RESULT 1387
ID ABU15177 standard; protein; 485 AA.
DE Protein encoded by Prokaryotic essential gene #704.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 485;
Best Local Similarity 29.0%; Pred. No. 8.5e+02;
RESULT 1388
ID ADS22830 standard; protein; 485 AA.
DE Bacterial polypeptide #11863.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 485;
Best Local Similarity 26.0%; Pred. No. 8.5e+02;
RESULT 1389
ID ABU35862 standard; protein; 490 AA.
DE Protein encoded by Prokaryotic essential gene #21389.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 490;
Best Local Similarity 23.6%; Pred. No. 8.7e+02;
RESULT 1390
ID ABU21209 standard; protein; 496 AA.
DE Protein encoded by Prokaryotic essential gene #6736.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 496;
Best Local Similarity 31.6%; Pred. No. 8.8e+02;

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RESULT 1391
ID ADP30474 standard; protein; 498 AA.
DE Human secreted protein SEQ ID #1241.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.0%; Score 60; DB 8; Length 498;
Best Local Similarity 36.0%; Pred. No. 8.8e+02;
RESULT 1392
ID ABG28672 standard; protein; 506 AA.
DE Novel human diagnostic protein #28663.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 506;
Best Local Similarity 27.8%; Pred. No. 9e+02;
RESULT 1393
ID ABU19802 standard; protein; 507 AA.
DE Protein encoded by Prokaryotic essential gene #5329.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 507;
Best Local Similarity 25.5%; Pred. No. 9.1e+02;
RESULT 1394
ID ABG94648 standard; protein; 511 AA.
DE Human NOV10b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 5; Length 511;
Best Local Similarity 26.2%; Pred. No. 9.1e+02;
RESULT 1395
ID ABB61121 standard; protein; 516 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10155.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.0%; Score 60; DB 4; Length 516;
Best Local Similarity 25.2%; Pred. No. 9.3e+02;
RESULT 1396
ID ABU15345 standard; protein; 530 AA.
DE Protein encoded by Prokaryotic essential gene #872.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 530;
Best Local Similarity 26.9%; Pred. No. 9.6e+02;
RESULT 1397
ID ABO71163 standard; protein; 549 AA.
DE Pseudomonas aeruginosa polypeptide #3338.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 60; DB 7; Length 549;
Best Local Similarity 23.0%; Pred. No. 1e+03;
RESULT 1398
ID ABB76947 standard; protein; 554 AA.
DE Acidocella sp phytase.
PN WO200238774-A2.
PD 16-MAY-2002.
PA (AVER-) AVENTIS ANIMAL NUTRITION SA.
Query Match 12.0%; Score 60; DB 5; Length 554;
Best Local Similarity 30.0%; Pred. No. 1e+03;
RESULT 1399
ID ADN25815 standard; protein; 554 AA.
DE Bacterial polypeptide #8468.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
RESULT 1400
ID AAE38766 standard; protein; 587 AA.
DE Rat 69624 protein sodium sulphate symporter domain.
PN US2002193582-A1.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.0%; Score 60; DB 7; Length 587;
Best Local Similarity 36.2%; Pred. No. 1.1e+03;
RESULT 1401
ID ADP55467 standard; protein; 592 AA.
DE Human novel polypeptide #31.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 12.0%; Score 60; DB 7; Length 592;
Best Local Similarity 26.8%; Pred. No. 1.1e+03;
RESULT 1402
ID AAR05589 standard; protein; 638 AA.
DE Acetylhydroxy acid synthetase (AHAS) from maize C3 genome.
PN EP360750-A.
PD 28-MAR-1990.
PA (CIBA-) CIBA GEIGY AG.
Query Match 12.0%; Score 60; DB 2; Length 638;
Best Local Similarity 23.0%; Pred. No. 1.2e+03;
RESULT 1403
ID AAB42426 standard; protein; 652 AA.
DE Human ORFX ORF2150 polypeptide sequence SEQ ID NO:4380.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 3; Length 652;
Best Local Similarity 26.6%; Pred. No. 1.3e+03;
RESULT 1404
ID ADS26132 standard; protein; 652 AA.
DE Bacterial polypeptide #15165.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 652;
Best Local Similarity 23.6%; Pred. No. 1.3e+03;
RESULT 1405
ID ADS25655 standard; protein; 652 AA.
DE Bacterial polypeptide #14688.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 652;
Best Local Similarity 23.6%; Pred. No. 1.3e+03;
RESULT 1406
ID ADS25373 standard; protein; 655 AA.
DE Bacterial polypeptide #14406.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 655;
Best Local Similarity 23.6%; Pred. No. 1.3e+03;
RESULT 1407
ID ADS22602 standard; protein; 656 AA.
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DE Bacterial polypeptide #11635.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.0%; Score 60; DB 8; Length 656;
Best Local Similarity 23.6%; Pred. No. 1.3e+03;
RESULT 1408
ID ABB62255 standard; protein; 680 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13557.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 60; DB 4; Length 680;
Best Local Similarity 32.8%; Pred. No. 1.3e+03;
RESULT 1409
ID ABU23341 standard; protein; 706 AA.
DE Protein encoded by Prokaryotic essential gene #7868.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 60; DB 6; Length 706;
Best Local Similarity 28.4%; Pred. No. 1.4e+03;
RESULT 1410
ID AAO14204 standard; protein; 707 AA.
DE Human transporter and ion channel TRICH-21.
PN WO200204520-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 60; DB 5; Length 707;
Best Local Similarity 29.5%; Pred. No. 1.4e+03;
RESULT 1411
ID ADD25157 standard; protein; 707 AA.
DE Fertility restorer protein #16.
PN WO2003006622-A2.
PD 23-JAN-2003.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
Query Match 12.0%; Score 60; DB 7; Length 707;
Best Local Similarity 26.3%; Pred. No. 1.4e+03;
RESULT 1412
ID ADN61172 standard; protein; 707 AA.
DE Radish nuclear fertility restorer Rfo protein SEQ ID NO:31.
PN WO2004006655-A2.
PD 22-JAN-2004.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 12.0%; Score 60; DB 8; Length 707;
Best Local Similarity 26.3%; Pred. No. 1.4e+03;
RESULT 1413
ID AD116618 standard; protein; 708 AA.
DE Human NOVX protein to treat human pathological conditions SeqId154.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 5; Length 708;
Best Local Similarity 29.5%; Pred. No. 1.4e+03;
RESULT 1414
ID ADN42272 standard; protein; 708 AA.
DE Human novel proteinNOV 41a.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERN/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LIL/) LI L.
PA (GANG/) GANGOLLI E A.

PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENM/) PENN C E A.
PA (FURT/) FURTA K.
PA (BURG/) BURGESS C E.
Query Match 12.0%; Score 60; DB 8; Length 708;
Best Local Similarity 29.5%; Pred. No. 1.4e+03;
RESULT 1415
ID AUB5408 standard; protein; 717 AA.
DE Human protein NOV6.
PN WO200210216-A2.
PD 07-FEB-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 5; Length 717;
Best Local Similarity 29.5%; Pred. No. 1.4e+03;
RESULT 1416
ID AAY43379 standard; protein; 722 AA.
DE M. catarrhalis strain 3 tbp2 protein.
PN WO952947-A2.
PD 21-OCT-1999.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 12.0%; Score 60; DB 2; Length 722;
Best Local Similarity 34.8%; Pred. No. 1.4e+03;
RESULT 1417
ID ABB67181 standard; protein; 747 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28335.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 60; DB 4; Length 747;
Best Local Similarity 30.1%; Pred. No. 1.5e+03;
RESULT 1418
ID AD116620 standard; protein; 761 AA.
DE Human NOVX protein to treat human pathological conditions SeqId156.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 60; DB 5; Length 761;
Best Local Similarity 29.5%; Pred. No. 1.5e+03;
RESULT 1419
ID ADN42274 standard; protein; 761 AA.
DE Human novel proteinNOV 41b.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERN/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LIL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENM/) PENN C E A.
PA (FURT/) FURTA K.

PA (GROS/) GROSSE W. M.
PA (ALSO/) ALSOBROOK J. P.
PA (LEPL/) LEPEL D. M.
PA (RIEG/) RIEGER D. K.
PA (BURG/) BURRESS C. E.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 761;
RESULT 1420
ID ADC31519 standard; protein; 771 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1601.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 771;
RESULT 1421
ID ADC31078 standard; protein; 776 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1160.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 776;
RESULT 1422
ID AD065222 standard; protein; 776 AA.
DE Novel human protein sequence #195.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 776;
RESULT 1423
ID AB02213 standard; protein; 798 AA.
DE S. pneumoniae type 4 strain protein from coding region #1791.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 798;
RESULT 1424
ID AD081821 standard; protein; 798 AA.
DE Human Na+/H+ exchange transporter.
PN WO2003062274-A1.
PD 31-JUL-2003.
PA (TAKE-) TAKEIDA CHEM IND LTD.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 798;
RESULT 1425
ID ADK46589 standard; protein; 798 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3104.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 798;
RESULT 1426
ID AAY55803 standard; protein; 804 AA.
DE S. pneumoniae priA polypeptide.
PN MO9661453-A2.
PD 02-DEC-1999.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 3; Length 804;
RESULT 1427
ID AD95849 standard; protein; 804 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4484.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 804;
RESULT 1428

ID ABR52748 standard; protein; 825 AA.
DE Protein sequence #SEQ ID 361.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 825;
RESULT 1429
ID ADK62052 standard; protein; 825 AA.
DE Disease treating protein complex-derived protein #152.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 12.0%; Score 60; DB 7; Length 825;
RESULT 1430
ID ABP73245 standard; protein; 907 AA.
DE Candida albicans essential protein SEQ ID NO 7082.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 907;
RESULT 1431
ID ABB58283 standard; protein; 935 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1641.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 935;
RESULT 1432
ID ADI46109 standard; protein; 1031 AA.
DE Single stranded nucleic acid cleavage method related protein #4.
PN WO200179481-A2.
PD 25-OCT-2001.
PA (DYAX-) DYAX CORP.
Query Match
Best Local Similarity 12.0%; Score 60; DB 5; Length 1031;
RESULT 1433
ID AB039615 standard; protein; 1035 AA.
DE Protein encoded by Prokaryotic essential gene #25142.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 6; Length 1035;
RESULT 1434
ID ABB57993 standard; protein; 1054 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 771.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 12.0%; Score 60; DB 4; Length 1054;
RESULT 1435
ID ADP31430 standard; protein; 1110 AA.
DE Human secreted protein SEQ ID #2197.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 1110;
RESULT 1436
ID ADN25166 standard; protein; 1174 AA.
DE Bacterial polypeptide #7819.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G. J.
PA (SLAT/) SLATER S. C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B. S.

Query Match 12.0%; Score 60; DB 8; Length 1174;
Best Local Similarity 30.5%; Pred. No. 2.7e+03;
RESULT 1437
ID ABB66003 standard; protein; 1184 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24801.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 60; DB 4; Length 1184;
Best Local Similarity 36.2%; Pred. No. 2.8e+03;
RESULT 1438
ID ABG24742 standard; protein; 1205 AA.
DE Novel human diagnostic protein #24733.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 1205;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1439
ID ABG10747 standard; protein; 1205 AA.
DE Novel human diagnostic protein #10738.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 1205;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1440
ID ADD71149 standard; protein; 1577 AA.
DE Human intracellular signalling molecule INTSIG-38 protein SEQ ID NO:38.
PN WO2003039348-A2.
PD 15-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 60; DB 7; Length 1577;
Best Local Similarity 27.4%; Pred. No. 4e+03;
RESULT 1441
ID ADQ91704 standard; protein; 1657 AA.
DE Polyketide synthase ORF13 protein, SEQ ID 27.
PN WO2004065401-A1.
PD 05-ANG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 8; Length 1657;
Best Local Similarity 26.3%; Pred. No. 4.3e+03;
RESULT 1442
ID ABG08232 standard; protein; 1700 AA.
DE Novel human diagnostic protein #8223.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 60; DB 4; Length 1700;
Best Local Similarity 30.5%; Pred. No. 4.4e+03;
RESULT 1443
ID ADJ70367 standard; protein; 1857 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2173.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 12.0%; Score 60; DB 7; Length 1857;
Best Local Similarity 27.4%; Pred. No. 5e+03;
RESULT 1444
ID AD019538 standard; protein; 1857 AA.
DE Human pro polypeptide #234.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.0%; Score 60; DB 8; Length 1857;
Best Local Similarity 27.4%; Pred. No. 5e+03;
RESULT 1445
ID ADP30882 standard; protein; 2187 AA.
DE Human secreted protein SEQ ID #1649.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 12.0%; Score 60; DB 8; Length 2187;
Best Local Similarity 39.5%; Pred. No. 6.2e+03;
RESULT 1446
ID AAB23832 standard; protein; 2625 AA.
DE Shewanella sp. SCRC-21406 (FERM BP-5979) ORF a protein SEQ ID NO:3.
PN JP2000217582-A.
PD 08-AUG-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (BIOT-) BIOINDUSTRY KYOKAI SH.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
Query Match 12.0%; Score 60; DB 3; Length 2625;
Best Local Similarity 26.7%; Pred. No. 7.9e+03;
RESULT 1447
ID AAB18637 standard; protein; 4551 AA.
DE Amino acid sequence of narbonolide synthase subunit 1 (PICAI).
PN US6117659-A.
PD 12-SEP-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 3; Length 4551;
Best Local Similarity 29.9%; Pred. No. 1.6e+04;
RESULT 1448
ID AAY67201 standard; protein; 4551 AA.
DE Narbonolide synthase subunit 1 (PICAI) protein sequence.
PN WO961599-A2.
PD 02-DEC-1999.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 3; Length 4551;
Best Local Similarity 29.9%; Pred. No. 1.6e+04;
RESULT 1449
ID ABG71661 standard; protein; 4551 AA.
DE S. venezuelae narbonolide synthase subunit 1, PICAI.
PN WO200297062-A2.
PD 05-DEC-2002.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 6; Length 4551;
Best Local Similarity 29.9%; Pred. No. 1.6e+04;
RESULT 1450
ID ADN09400 standard; protein; 4551 AA.
DE S. venezuelae narbonolide synthase subunit 1 (PICAI).
PN US6509455-B1.
PD 21-JAN-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 12.0%; Score 60; DB 6; Length 4551;
Best Local Similarity 29.9%; Pred. No. 1.6e+04;
RESULT 1451
ID ADH53444 standard; protein; 4551 AA.
DE Streptomyces venezuelae narbonolide synthase subunit 1 protein, PICAI.
PN US2003162262-A1.
PD 28-AUG-2003.
PA (ASHL/) ASHLEY G.
PA (BETL/) BETLACH M.C.
PA (BETL/) BETLACH M.
PA (MCDA/) MCDANIEL R.
PA (TANG/) TANG L.
Query Match 12.0%; Score 60; DB 7; Length 4551;
Best Local Similarity 29.9%; Pred. No. 1.6e+04;
RESULT 1452
ID AAY77200 standard; protein; 4613 AA.
DE S. venezuelae pik (macrolide biosynthesis) gene cluster protein #1.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 12.0%; Score 60; DB 3; Length 4613;
Best Local Similarity 29.9%; Pred. No. 1.7e+04;
RESULT 1453
ID AAY77192 standard; protein; 4613 AA.
DE S. venezuelae macrolide biosynthetic enzyme Pikai, SEQ ID NO:31.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 12.0%; Score 60; DB 3; Length 4613;
Best Local Similarity 29.9%; Pred. No. 1.7e+04;
RESULT 1454

ID ADL91916 standard; protein; 4613 AA.
DE Streptomyces macrolide biosynthetic protein - PIKR2.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 4613;
RESULT 1455
ID AAM19629 standard; protein; 4630 AA.
DE Streptomyces venezuelae polyketide synthase.
PN WO9722711-A1.
PD 26-JUN-1997.
PA (MINU) UNIV MINNESOTA.
Query Match
Best Local Similarity 12.0%; Score 60; DB 2; Length 4630;
RESULT 1456
ID ADL91934 standard; protein; 11877 AA.
DE Streptomyces venezuelae pik gene cluster protein.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 11877;
RESULT 1457
ID AAY77180 standard; protein; 12199 AA.
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match
Best Local Similarity 12.0%; Score 60; DB 3; Length 12199;
RESULT 1458
ID ABP04991 standard; protein; 77 AA.
DE Human ORFX protein sequence SEQ ID NO:9964.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 5; Length 77;
RESULT 1459
ID AAY04746 standard; protein; 100 AA.
DE Mycobacterium species protein sequence 1#4.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 100;
RESULT 1460
ID ADJ50224 standard; protein; 124 AA.
DE Oil-associated gene related protein #1724.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 124;
RESULT 1461
ID ADJ49790 standard; protein; 132 AA.
DE Oil-associated gene related protein #1290.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.

PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 132;
RESULT 1462
ID AAY04897 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 28.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1463
ID AAY04754 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 2#3.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1464
ID AAY04750 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 1D.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1465
ID AAB52478 standard; protein; 136 AA.
DE Mycobacterium tuberculosis secreted protein #43.
PN WO200066143-A1.
PD 09-NOV-2000.
PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 136;
RESULT 1466
ID ABG31899 standard; protein; 148 AA.
DE Novel human diagnostic protein #13890.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1467
ID ABG00067 standard; protein; 148 AA.
DE Novel human diagnostic protein #58.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1468
ID ABG02758 standard; protein; 148 AA.
DE Novel human diagnostic protein #2749.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1469
ID AAY04751 standard; protein; 165 AA.
DE Mycobacterium species protein sequence 1F.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 165;
RESULT 1470
ID ABB67828 standard; protein; 176 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30276.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 11.9%; Score 59.5; DB 4; Length 176;
Best Local Similarity 29.0%; Pred. No. 2.6e+02;
RESULT 1471
ID AAY71042 standard; protein; 217 AA.
DE Streptococcus pyogenes strain SF370 full-length GRAB protein.
PN MO20026240-A2.
PD 11-MAY-2000.
PA (ACTI-) ACTINOVA LTD.
Query Match 11.9%; Score 59.5; DB 3; Length 217;
Best Local Similarity 29.9%; Pred. No. 3.4e+02;
RESULT 1472
ID ABP30013 standard; protein; 217 AA.
DE Streptococcus polypeptide SEQ ID NO 9202.
PN MO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 11.9%; Score 59.5; DB 5; Length 217;
Best Local Similarity 29.9%; Pred. No. 3.4e+02;
RESULT 1473
ID ADR83937 standard; protein; 217 AA.
DE S. pyogenes hyperimmune system reactive antigen Spy1357.
PN MO2004078907-A2.
PD 16-SEP-2004.
PA (INTE-) INTERCELL AG.
Query Match 11.9%; Score 59.5; DB 8; Length 217;
Best Local Similarity 29.9%; Pred. No. 3.4e+02;
RESULT 1474
ID AAY73464 standard; protein; 220 AA.
DE Human secreted protein clone y14_1 protein sequence SEQ ID NO:150.
PN MO958642-A2.
PD 18-NOV-1999.
PA (GENM-) GENETICS INST INC.
Query Match 11.9%; Score 59.5; DB 3; Length 220;
Best Local Similarity 28.6%; Pred. No. 3.4e+02;
RESULT 1475
ID ABB76449 standard; protein; 252 AA.
DE Daf-4 bone morphogenetic protein receptor extracellular domain.
PN MO200239118-A1.
PD 16-MAY-2002.
PA (THRA-) THRASOS INC.
Query Match 11.9%; Score 59.5; DB 5; Length 252;
Best Local Similarity 26.7%; Pred. No. 4.1e+02;
RESULT 1476
ID ABU33941 standard; protein; 256 AA.
DE Protein encoded by prokaryotic essential gene #19468.
PN MO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 59.5; DB 6; Length 256;
Best Local Similarity 26.5%; Pred. No. 4.2e+02;
RESULT 1477
ID AAY71043 standard; protein; 259 AA.
DE Streptococcus pyogenes strain KTL9 partial GRAB protein.
PN MO200026240-A2.
PD 11-MAY-2000.
PA (ACTI-) ACTINOVA LTD.
Query Match 11.9%; Score 59.5; DB 3; Length 259;
Best Local Similarity 29.9%; Pred. No. 4.3e+02;
RESULT 1478
ID ADR43144 standard; protein; 295 AA.
DE IPT-like structural protein #203.
PN MO2004074442-A2.
PD 02-SEP-2004.
PA (MONS) MONGANNO TECHNOLOGY LLC.
Query Match 11.9%; Score 59.5; DB 8; Length 295;
Best Local Similarity 25.4%; Pred. No. 5.1e+02;
RESULT 1479
ID ABO61089 standard; protein; 302 AA.
DE Klebsiella pneumoniae polypeptide seqid 7606.
PN US6610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 59.5; DB 7; Length 302;
Best Local Similarity 29.5%; Pred. No. 5.2e+02;
RESULT 1480
ID AAR31020 standard; protein; 307 AA.
DE Grass pollen allergen, KRG 60.
PN CA2066801-A.
PD 27-OCT-1992.
PA (MOHA/) MOHAPATRA S S.
Query Match 11.9%; Score 59.5; DB 2; Length 307;
Best Local Similarity 29.3%; Pred. No. 5.3e+02;
RESULT 1481
ID AAG72623 standard; protein; 317 AA.
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2304.
PN MO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 11.9%; Score 59.5; DB 4; Length 317;
Best Local Similarity 34.3%; Pred. No. 5.6e+02;
RESULT 1482
ID AAY04747 standard; protein; 320 AA.
DE Mycobacterium species protein sequence 1A'.
PN MO9909186-A2.
PD 25-FEB-1999.
PA (INSP-) INST PASTEUR.
Query Match 11.9%; Score 59.5; DB 2; Length 320;
Best Local Similarity 26.9%; Pred. No. 5.6e+02;
RESULT 1483
ID ABU28912 standard; protein; 327 AA.
DE Protein encoded by prokaryotic essential gene #14439.
PN MO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 59.5; DB 6; Length 327;
Best Local Similarity 23.2%; Pred. No. 5.8e+02;
RESULT 1484
ID ADC01360 standard; protein; 327 AA.
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 1405.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 11.9%; Score 59.5; DB 7; Length 327;
Best Local Similarity 23.2%; Pred. No. 5.8e+02;
RESULT 1485
ID ADS27824 standard; protein; 328 AA.
DE Bacterial polypeptide #16857.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 11.9%; Score 59.5; DB 8; Length 328;
Best Local Similarity 26.3%; Pred. No. 5.8e+02;
RESULT 1486
ID ABR56731 standard; protein; 334 AA.
DE Human secreted protein SSCP-6 SEQ ID NO:6.
PN MO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.9%; Score 59.5; DB 6; Length 334;
Best Local Similarity 34.8%; Pred. No. 6e+02;
RESULT 1487
ID ADE28661 standard; protein; 334 AA.
DE Human NOV13a protein - SEQ ID 38.
PN MO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.9%; Score 59.5; DB 7; Length 334;
Best Local Similarity 34.8%; Pred. No. 6e+02;
RESULT 1488

ID ADM93406 standard; protein; 334 AA.
DE Human NOVX polypeptide #19.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E. P.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIT/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTEBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIMW/) JI W.
PA (KERU/) KERUDA R.
PA (KIRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCOU/) MCCOENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENY/) PENNA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARKLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOI/) TWOMLOW N.
PA (VERN/) VERNIST C A M.
PA (ZERR/) ZERRHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 334;
RESULT 1489
ID ADR13777 standard; protein; 336 AA.
DE Amidase, SEQ ID 114.
PN WO2004069848-A2.
PD 19-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 336;
RESULT 1490
ID AAG52436 standard; protein; 337 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66653.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 3; Length 337;
DE Mouse alcohol dehydrogenase #1.

RESULT 1491
ID ABB66995 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide seq ID NO 27777.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 339;
RESULT 1492
ID ABO66983 standard; protein; 352 AA.
DE Klebsiella pneumoniae polypeptide seqid 13500.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 7; Length 352;
RESULT 1493
ID ADG22336 standard; protein; 353 AA.
DE Cyanophage S-2L encoded protein #81.
PN FR839079-A1.
PD 31-OCT-2003.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 353;
RESULT 1494
ID ADQ94412 standard; protein; 367 AA.
DE E. coli Aspartate semialdehyde dehydrogenase.
PN WO2004058954-A2.
PD 15-JUL-2004.
PA (AFPI-) AFFINITUM PHARM INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 367;
RESULT 1495
ID ADS45159 standard; protein; 367 AA.
DE Bacterial polypeptide #23589.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 367;
RESULT 1496
ID AAV41496 standard; protein; 368 AA.
DE Fragment of human secreted protein encoded by gene 70.
PN WO9947540-A1.
PD 23-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 368;
RESULT 1497
ID ADM76949 standard; protein; 368 AA.
DE ATG-act protein sequence.
PN WO2004020643-A2.
PD 11-MAR-2004.
PA (UNIW) UNIV WASHINGTON.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 368;
RESULT 1498
ID ADM76946 standard; protein; 368 AA.
DE GTP-act protein sequence.
PN WO2004020643-A2.
PD 11-MAR-2004.
PA (UNIW) UNIV WASHINGTON.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 368;
RESULT 1499
ID AAV43986 standard; protein; 374 AA.
DE Mouse alcohol dehydrogenase #1.

PN US5958784-A.
PD 28-SEP-1999.
PA (BENN/) BENNER S A.
Query Match 11.9%; Score 59.5; DB 2; Length 374;
Best Local Similarity 29.3%; Pred. No. 6.9e+02;
RESULT 1500
ID ABU22527 standard; protein; 380 AA.
DE Protein encoded by Prokaryotic essential gene #8054.
PN WO200277183-A2.
PD 03-OCT-2002
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 59.5; DB 6; Length 380;
Best Local Similarity 28.0%; Pred. No. 7.1e+02;

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Run on: March 8, 2005, 04:41:24 ; Search time 436 Seconds
GenCore version 5.1.6
(without alignments)
7739.111 Million cell updates/sec

Title: US-09-989-731-407

Perfect score: 570

Sequence: 1 gcgagaccg99cataagaa.....aaaaaaaaaaaaaaaa 570
IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0
4390206 segs, 2959870667 residues
8780412

Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

- 1: geneseqn16dec04.*
- 2: geneseqn19806.*
- 3: geneseqn19908.*
- 4: geneseqn20008.*
- 5: geneseqn2001as.*
- 6: geneseqn2002as.*
- 7: geneseqn2003as.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID /	AAZ65103	standard;	CDNA;	570	BP.	
DE	Membrane-bound protein PRO1245	encoding	CDNA.			
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 3;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 2						
ID /	AAFA4249	standard;	CDNA;	570	BP.	
DE	Human PRO1245 (UNC629)	nucleotide sequence	SEQ ID NO:407.			
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 5;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 3						
ID	ACA64431	standard;	CDNA;	570	BP.	
DE	Novel human secreted and transmembrane protein PRO1245	CDNA.				
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 4						
ID	ABX80890	standard;	CDNA;	570	BP.	
DE	Human secreted/transmembrane protein CDNA, #163.					
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 5						
ID	ACD44399	standard;	CDNA;	570	BP.	
DE	CDNA encoding human PRO1245 polypeptide.					
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	

Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 6						
ID	ABX79570	standard;	CDNA;	570	BP.	
DE	Human secreted/transmembrane protein CDNA, #163.					
PN	US2002142961-A1.					
PD	03-OCT-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 7						
ID	ACA93591	standard;	CDNA;	570	BP.	
DE	Novel human secreted and transmembrane protein PRO1245	CDNA.				
PN	US2003022187-A1.					
PD	30-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 8						
ID	ABX81273	standard;	DNA;	570	BP.	
DE	Novel human secreted or transmembrane protein PRO1358	DNA.				
PN	US2003027985-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 9						
ID	ACA93089	standard;	CDNA;	570	BP.	
DE	Novel human secreted and transmembrane protein PRO1245	CDNA.				
PN	US2003017476-A1.					
PD	23-JUN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 10						
ID	ABX17173	standard;	CDNA;	570	BP.	
DE	Human PRO polynucleotide #127.					
PN	US2002123463-A1.					
PD	05-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 8;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 11						
ID	ACA68028	standard;	CDNA;	570	BP.	
DE	Novel human secreted and transmembrane protein PRO1245	CDNA.				
PN	US2002177164-A1.					
PD	28-NOV-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 9;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 12						
ID	ACA88477	standard;	CDNA;	570	BP.	
DE	Human secreted and transmembrane polypeptide PRO1245	CDNA.				
PN	US2002197615-A1.					
PD	26-DEC-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 9;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 13						
ID	ACD81984	standard;	CDNA;	570	BP.	
DE	CDNA encoding human PRO1245 polypeptide.					
PN	US2003017981-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 9;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 14						
ID	ADA37918	standard;	CDNA;	570	BP.	
DE	Human cDNA encoding secreted/transmembrane protein PRO1245.					
PN	US2003008297-A1.					
PD	09-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 570;	DB 9;	Length 570;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-89;			
RESULT 15						
ID	ADA21604	standard;	CDNA;	570	BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO1245.					
PN	US2003054404-A1.					

PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 16
ID ADA10391 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1245.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 17
ID ADA17935 standard; cDNA; 570 BP.
DE cDNA encoding human PRO1245 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 18
ID ADA28043 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 19
ID ADA94623 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 20
ID ADA38948 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 21
ID ADA92969 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 22
ID ACH65545 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 23
ID ADA22530 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1245.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 24
ID ACD39535 standard; cDNA; 570 BP.
DE Human cDNA encoding PRO1358.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 25
ID ADA06696 standard; cDNA; 570 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #127.
PN US2003059638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
PD 100.0%; Pred. No. 5.5e-89;

RESULT 26
ID ADA93389 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 27
ID ADB96415 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;
RESULT 28
ID ADC57887 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 29
ID ADC55251 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 30
ID ADC12118 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 31
ID ADC65640 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 32
ID ADC07595 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 33
ID ADC11585 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 34
ID ADC14707 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 35
ID ADD06239 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;
RESULT 36
ID ADC82064 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.

PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 37
ID ADD07706 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 38
ID ADC82597 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 39
ID ADD08777 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 40
ID ADD07026 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 41
ID ADC63273 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 42
ID ADD55380 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003077553-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 43
ID ADD56338 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 44
ID ADD54776 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 45
ID ADE26930 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 46
ID ADE26397 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.

PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 47
ID ADF67334 standard; cDNA; 570 BP.
DE Human PRO1245 nucleotide sequence SEQ ID NO:407.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 48
ID ADI35588 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 49
ID ADI00081 standard; cDNA; 570 BP.
DE Novel human secreted and transmembrane protein PRO1245 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 50
ID ABX77974 standard; cDNA; 570 BP.
DE Human PRO polynucleotide #127.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 51
ID ABX80386 standard; DNA; 570 BP.
DE Novel human secreted or transmembrane protein PRO1358 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 52
ID ACA69292 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 53
ID ABX90363 standard; cDNA; 570 BP.
DE Human secreted/transmembrane protein cDNA, #163.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 54
ID ABX64209 standard; cDNA; 570 BP.
DE cDNA encoding human PRO1245 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 570; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 55
ID ADF35533 standard; cDNA; 570 BP.
DE cDNA encoding human PRO1245 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 570; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 56
ID ADG11783 standard; cDNA; 570 BP.

DE cDNA encoding human PRO1245 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 57
ID ADH19653 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 58
ID ADH21146 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 59
ID ADH20186 standard; cDNA; 570 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1245.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 570; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e-89;
RESULT 60
ID ABR40267 standard; cDNA; 569 BP.
DE cDNA encoding human PRO1245 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH) GENENTECH INC.
Query Match 99.8%; Score 569; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.2e-89;
RESULT 61
ID ADJ37308 standard; cDNA; 569 BP.
DE Human tumour therapy associated PRO1245 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.8%; Score 569; DB 10; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.2e-89;
RESULT 62
ID ADG68232 standard; cDNA; 569 BP.
DE Human PRO polypeptide cDNA #14.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.8%; Score 569; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.2e-89;
RESULT 63
ID AAZ29723 standard; DNA; 543 BP.
DE Human lung specific gene lng107.
PN WO960160-A1.
PD 25-NOV-1999.
PA (DIAD-) DIADEXUS LLC.
Query Match 92.8%; Score 529; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 6e-82;
RESULT 64
ID AAZ98173 standard; cDNA; 543 BP.
DE Human signal peptide containing protein HSP-65 cDNA SEQ ID NO:199.
PN WO200006010-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 92.8%; Score 529; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 6e-82;
RESULT 65
ID ADB39936 standard; cDNA; 561 BP.
DE Human lung disorder-related cDNA - SEQ ID 6.
PN US2003124580-A1.

PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 91.8%; Score 523; DB 10; Length 561;
Best Local Similarity 100.0%; Pred. No. 6.5e-81;
RESULT 66
ID AAV54621 standard; cDNA; 519 BP.
DE LUI05 polypeptide encoding cDNA clone 1327836IH.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 91.1%; Score 519; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 3.1e-80;
RESULT 67
ID AAV54620 standard; cDNA; 562 BP.
DE LUI05 specific consensus polynucleotide sequence.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 91.0%; Score 518.6; DB 2; Length 562;
Best Local Similarity 99.8%; Pred. No. 3.7e-80;
RESULT 68
ID ADP45231 standard; DNA; 527 BP.
DE Human lung cancer specific DNA #2.
PN US2004101876-A1.
PD 27-MAY-2004.
PA (MINT/) MINTZ L.
PA (XIEH/) XIE H.
PA (DAHA/) DAFARI D.
PA (LEVA/) LEVANON E.
PA (FREI/) FREILICH S.
PA (BECK/) BECK N.
PA (ZHUW/) ZHU W.
PA (MASS/) WASSERMAN A.
PA (HERM/) HERMESH C.
PA (AZAR/) AZAR I.
PA (BERN/) BERNSTEIN J.
PA (SORE/) SOREK R.
Query Match 90.9%; Score 518; DB 12; Length 527;
Best Local Similarity 100.0%; Pred. No. 4.7e-80;
RESULT 69
ID ADU75215 standard; DNA; 461 BP.
DE Marker gene SEQ ID NO:467.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 80.3%; Score 457.8; DB 12; Length 461;
Best Local Similarity 99.6%; Pred. No. 1e-69;
RESULT 70
ID ABT10080 standard; cDNA; 526 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 214.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 72.1%; Score 411.2; DB 6; Length 526;
Best Local Similarity 90.7%; Pred. No. 1e-61;
RESULT 71
ID ADI36344 standard; cDNA; 312 BP.
DE Full-length hIN-1 encoding cDNA, seq id 3.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DNA PARBER CANCER INST INC.
Query Match 54.2%; Score 308.8; DB 10; Length 312;
Best Local Similarity 99.4%; Pred. No. 3.8e-44;
RESULT 72
ID ABI66623 standard; DNA; 380 BP.
DE lung cancer related gene sequence SEQ ID NO:4960.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 51.5%; Score 293.4; DB 6; Length 380;
Best Local Similarity 91.9%; Pred. No. 1.7e-41;
RESULT 73

ID AD136345 standard; cDNA; 258 BP.
DE Mature hIN-1 encoding cDNA, seq id 4.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.9%; Score 256; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 4.4e-35;
RESULT 74
ID AD136346 standard; cDNA; 252 BP.
DE Mature hIN-1 encoding cDNA, seq id 23.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.2%; Score 252; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
RESULT 75
ID AAV54617 standard; cDNA; 244 BP.
DE LUI05 specific polynucleotide sequence from clone 1327836.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 42.4%; Score 241.4; DB 2; Length 244;
Best Local Similarity 99.2%; Pred. No. 1.4e-32;
RESULT 76
ID AAV54618 standard; cDNA; 225 BP.
DE LUI05 specific polynucleotide sequence from clone 1605935.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 39.5%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.3e-30;
RESULT 77
ID ACH19647 standard; cDNA; 416 BP.
DE Human adult lung cDNA #650.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA) DRMANAC R T.
PA (LABA) LABAT I.
PA (STAC) STACHE-CRAIN B.
PA (DICK) DICKSON M C.
PA (JONE) JONES L W.
Query Match 29.5%; Score 168.4; DB 9; Length 416;
Best Local Similarity 99.4%; Pred. No. 5.1e-20;
RESULT 78
ID AAV54616 standard; cDNA; 190 BP.
DE LUI05 specific polynucleotide sequence from clone 3353867.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 25.3%; Score 144; DB 2; Length 190;
Best Local Similarity 98.0%; Pred. No. 7.5e-16;
RESULT 79
ID ADM83730 standard; DNA; 1794 BP.
DE Human high in normal-1 (HIN-1) cDNA.
PN US200318783-A1.
PD 24-JUL-2003.
PA (SUKU) SUKUMAR S.
PA (EVRO) EVRON E.
PA (DOOL) DOOLEY W C.
PA (SACC) SACCCHI N.
PA (DAVI) DAVIDSON N.
PA (PACK) PACKLER M J.
Query Match 21.8%; Score 124; DB 11; Length 1794;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
RESULT 80
ID AAI86394 standard; cDNA; 404 BP.
DE Human polynucleotide seq ID NO 6454.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE) HYSEQ INC.
Query Match 20.4%; Score 116; DB 4; Length 404;

Best Local Similarity 88.7%; Pred. No. 5.1e-11;
RESULT 81
ID AAV54619 standard; cDNA; 114 BP.
DE LUI05 specific polynucleotide sequence from clone 811640.
PN WO9833926-A1.
PD 06-AUG-1998.
PA (ABBO) ABBOTT LAB.
Query Match 20.0%; Score 114; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 82
ID AD136318 standard; cDNA; 312 BP.
DE Full-length hIN-1 encoding cDNA, seq id 7.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 19.3%; Score 109.8; DB 10; Length 312;
Best Local Similarity 66.1%; Pred. No. 5.8e-10;
RESULT 83
ID AD136319 standard; cDNA; 255 BP.
DE Mature hIN-1 encoding cDNA, seq id 8.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 16.2%; Score 92.6; DB 10; Length 255;
Best Local Similarity 64.2%; Pred. No. 5.1e-07;
RESULT 84
ID ABT06542 standard; DNA; 1794 BP.
DE Human HIN-1 coding sequence.
PN WO200259347-A2.
PD 01-APR-2002.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 16.0%; Score 91.4; DB 6; Length 1794;
Best Local Similarity 56.9%; Pred. No. 9.3e-07;
RESULT 85
ID AD136320 standard; cDNA; 249 BP.
DE Mature hIN-1 encoding cDNA, seq id 25.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.8%; Score 90; DB 10; Length 249;
Best Local Similarity 64.5%; Pred. No. 1.4e-06;
RESULT 86
ID AD136325 standard; cDNA; 279 BP.
DE Full-length hIN-1 encoding cDNA, seq id 20.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.6%; Score 88.8; DB 10; Length 279;
Best Local Similarity 63.1%; Pred. No. 2.3e-06;
RESULT 87
ID AD136327 standard; cDNA; 249 BP.
DE Mature hIN-1 encoding cDNA, seq id 26.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.3%; Score 87.2; DB 10; Length 249;
Best Local Similarity 65.5%; Pred. No. 4.3e-06;
RESULT 88
ID AD136324 standard; DNA; 551 BP.
DE hIN-1 promoter sequence, seq id 19.
PN WO200268673-A2.
PD 06-SEP-2002.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.7%; Score 78; DB 10; Length 551;
Best Local Similarity 100.0%; Pred. No. 0.00017;
RESULT 89
ID ADP10592 standard; DNA; 200 BP.

DE Reference mRNA sequences for marker probe #269.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 12.5%; Score 71; DB 12; Length 200;
RESULT 90
ID AAX26196 standard; DNA; 1613 BP.
DE DNA sequence of glycosyltransferase gene.
PN JP11056373-A.
PD 02-MAR-1999.
PA (FURU/) FURUKAWA K.
Query Match
Best Local Similarity 12.2%; Score 69.4; DB 2; Length 1613;
RESULT 91
ID ACN52874 standard; cDNA; 589 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H4, SEQ:7655.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 12.1%; Score 69; DB 13; Length 589;
RESULT 92
ID AAT79634 standard; DNA; 1898 BP.
DE DNA encoding human ubiquituous nuclear receptor polypeptide.
PN US5639616-A.
PD 17-JUN-1997.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 12.1%; Score 69; DB 2; Length 1898;
RESULT 93
ID AB190773 standard; cDNA; 1360 BP.
DE Human polynucleotide SEQ ID NO 1335.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.0%; Score 68.4; DB 6; Length 1360;
RESULT 94
ID AB278096 standard; cDNA; 862 BP.
DE Human breast specific nucleic acid #110.
PN WO200268645-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 11.9%; Score 68; DB 6; Length 862;
RESULT 95
ID ACN56642 standard; cDNA; 598 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 11.9%; Score 67.6; DB 13; Length 598;
RESULT 96
ID AAD05580 standard; cDNA; 2187 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HRAEH37, SEQ ID NO:12.
PN WO200134627-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.9%; Score 67.6; DB 4; Length 2187;
RESULT 97
ID ACN56129 standard; cDNA; 496 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-C10, SEQ:10910.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 496;
RESULT 98
ID AAC59305 standard; cDNA; 566 BP.
DE Human secreted protein cDNA #29.
PN WO200056753-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 3; Length 566;
RESULT 99
ID ADA97967 standard; cDNA; 566 BP.
DE Human secreted protein cDNA sequence #61.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 8; Length 566;
RESULT 100
ID ADA43873 standard; cDNA; 566 BP.
DE Human secreted protein cDNA SEQ ID 61.
PN WO200300865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 8; Length 566;
RESULT 101
ID ADC20123 standard; DNA; 566 BP.
DE Human secreted protein coding sequence #62.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 10; Length 566;
RESULT 102
ID ADP10581 standard; DNA; 566 BP.
DE Human secreted protein encoding sequence #34.
PN WO20029085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 10; Length 566;
RESULT 103
ID ACN52093 standard; cDNA; 579 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-C7, SEQ:6874.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 579;
RESULT 104
ID ADR14449 standard; DNA; 1460 BP.
DE Human NF-kappaB pathway-associated gene SeqID450.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 1460;
RESULT 105
ID AAO88760 standard; DNA; 1813 BP.
DE Human ubiquitous nuclear receptor protein DNA.
PN WO9513373-A1.
PD 18-MAY-1995.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 2; Length 1813;
RESULT 106
ID AAO88760 standard; DNA; 1813 BP.
DE Human ubiquitous nuclear receptor protein DNA.
PN WO9513373-A1.
PD 18-MAY-1995.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 11.8%; Score 67.4; DB 2; Length 1813;

RESULT 106
ID ACN4862 standard; cDNA; 516 BP.
DE Cotton primed seed EST Clone ID: LIB3825-027-Q6-N6-H7, SEQ:3643.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.8%; Score 67.2; DB 13; Length 516;
Best Local Similarity 66.2%; Pred. No. 0.012;
RESULT 107
ID ADI62837 standard; cDNA; 733 BP.
DE Human apoptosis-associated cDNA SEQ ID 280.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 11.8%; Score 67; DB 10; Length 733;
Best Local Similarity 54.7%; Pred. No. 0.014;
RESULT 108
ID ADI62835 standard; cDNA; 733 BP.
DE Human apoptosis-associated cDNA SEQ ID 278.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 11.8%; Score 67; DB 10; Length 733;
Best Local Similarity 54.7%; Pred. No. 0.014;
RESULT 109
ID ABT1910 standard; DNA; 1375 BP.
DE Human breast cancer / ovarian cancer related coding sequence #17.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.8%; Score 67; DB 10; Length 1375;
Best Local Similarity 61.3%; Pred. No. 0.014;
RESULT 110
ID ABZ82489 standard; cDNA; 805 BP.
DE Human secreted protein cDNA #SEQ ID 36.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.7%; Score 66.8; DB 6; Length 805;
Best Local Similarity 81.9%; Pred. No. 0.015;
RESULT 111
ID ACN49708 standard; cDNA; 554 BP.
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.7%; Score 66.6; DB 13; Length 554;
Best Local Similarity 67.9%; Pred. No. 0.016;
RESULT 112
ID ACN45287 standard; cDNA; 573 BP.
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-N6-H7, SEQ:68.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.7%; Score 66.6; DB 13; Length 573;
Best Local Similarity 71.9%; Pred. No. 0.016;
RESULT 113
ID ABK3926 standard; DNA; 9884 BP.
DE Human DNA for staging of Astrocytomas, complement, #4.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.7%; Score 66.6; DB 6; Length 9884;
Best Local Similarity 71.9%; Pred. No. 0.019;

RESULT 114
ID ADA20341 standard; DNA; 9884 BP.
DE Prostate tumour related genomic DNA complement sample #3.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.7%; Score 66.6; DB 8; Length 9884;
Best Local Similarity 71.9%; Pred. No. 0.019;
RESULT 115
ID ADA84148 standard; DNA; 9884 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:6.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.7%; Score 66.6; DB 8; Length 9884;
Best Local Similarity 71.9%; Pred. No. 0.019;
RESULT 116
ID ACN51610 standard; cDNA; 579 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-B6, SEQ:6391.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.6%; Score 66.4; DB 13; Length 579;
Best Local Similarity 79.0%; Pred. No. 0.017;
RESULT 117
ID ADQ23300 standard; DNA; 1744 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6120.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.5%; Score 65.8; DB 12; Length 1744;
Best Local Similarity 85.9%; Pred. No. 0.023;
RESULT 118
ID ABX39555 standard; cDNA; 383 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4720.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 11.5%; Score 65.6; DB 8; Length 383;
Best Local Similarity 64.5%; Pred. No. 0.023;
RESULT 119
ID ADN39690 standard; cDNA; 550 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:662.
PN WO2003042651-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.5%; Score 65.6; DB 11; Length 550;
Best Local Similarity 51.5%; Pred. No. 0.023;
RESULT 120
ID AAAS6893 standard; cDNA; 646 BP.
DE cDNA sequence of a novel gene associated with insulin synthesis.
PN WO200040722-A2.
PD 13-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 11.5%; Score 65.4; DB 3; Length 646;
Best Local Similarity 63.9%; Pred. No. 0.026;
RESULT 121
ID AAD42580 standard; cDNA; 646 BP.
DE Human cDNA #2 co-expressed with collagenase gene.
PN US2002077309-A1.
PD 20-JUN-2002.
PA (WALK/) WALKER M G.
PA (VOLK/) VOLKMUH W.
PA (KLIN/) KLINGLER T M.
Query Match 11.5%; Score 65.4; DB 6; Length 646;
Best Local Similarity 63.9%; Pred. No. 0.026;
RESULT 122

ID ADC06744 standard; cDNA; 1723 BP.
DE Human inositol hexakisphosphate kinase 1 cDNA.
PN W02003066087-A2.
PD 14-AUG-2003.
PA (DEVE-) DEVELOPGEN ENTWICKLUNGSBIOLOGISC AG.
Query Match 11.5%; Score 65.4; DB 10; Length 1723;
Best Local Similarity 75.7%; Pred. No. 0.027;
RESULT 123
ID AAF18317 standard; DNA; 1607 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 336.
PN W0200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 65; DB 3; Length 1607;
Best Local Similarity 85.5%; Pred. No. 0.032;
RESULT 124
ID AAS29076 standard; cDNA; 316 BP.
DE cDNA encoding for human DNA-binding protein #47.
PN W0200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 5; Length 316;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 125
ID ABS68216 standard; cDNA; 316 BP.
DE cDNA encoding human DNA-binding protein #47.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 11.4%; Score 64.8; DB 6; Length 316;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 126
ID ADC25210 standard; cDNA; 316 BP.
DE Human cDNA from extracellular matrix gene 47.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 4; Length 316;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 127
ID AAV59298 standard; cDNA; 326 BP.
DE Human prostate expression marker cDNA 59289.
PN W0200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 64.8; DB 5; Length 326;
Best Local Similarity 85.7%; Pred. No. 0.031;
RESULT 128
ID AAS35460 standard; cDNA; 362 BP.
DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID No 345.
PN W0200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 4; Length 362;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 129
ID AAS29148 standard; cDNA; 362 BP.
DE cDNA encoding for human DNA-binding protein #119.
PN W0200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 5; Length 362;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 130
ID ABS68288 standard; cDNA; 362 BP.
DE cDNA encoding human DNA-binding protein #119.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
Query Match 11.4%; Score 64.8; DB 4; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 131
ID ADC25282 standard; cDNA; 362 BP.
DE Human cDNA from extracellular matrix gene 119.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 10; Length 362;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 132
ID ADE4539 standard; cDNA; 362 BP.
DE Human cardiovascular system related polynucleotide #335.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 13; Length 362;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 133
ID ADJ06957 standard; DNA; 362 BP.
DE Human cardiovascular system associated gene SeqID345.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 13; Length 362;
Best Local Similarity 75.0%; Pred. No. 0.031;
RESULT 134
ID ACN62126 standard; cDNA; 483 BP.
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-N6-D4, SEQ:2061.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FING/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.4%; Score 64.8; DB 13; Length 483;
Best Local Similarity 72.4%; Pred. No. 0.032;
RESULT 135
ID ACN62126 standard; cDNA; 533 BP.
DE Cotton gynoeclium tissue EST Clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FING/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.4%; Score 64.8; DB 13; Length 533;
Best Local Similarity 78.0%; Pred. No. 0.032;
RESULT 136
ID AAD02075 standard; cDNA; 1043 BP.
DE Human encoding human pituitary hormone, pituitrone.
PN W0200066778-A1.
PD 09-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 3; Length 1043;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 137
ID AA298064 standard; cDNA; 1050 BP.
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:58.
PN W0200004140-A1.
PD 27-JAN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 3; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 138
ID AAD1677 standard; cDNA; 1050 BP.
DE Human secreted protein-encoding gene 48 cDNA clone HKGDL36, SEQ ID NO:58.
PN W0200151504-A1.
PD 19-JUL-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 4; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;

RESULT 139
ID ABK69773 standard; cDNA; 1050 BP.
DE Human secreted protein gene 48.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 6; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 140
ID ACC50758 standard; cDNA; 1050 BP.
DE Human secreted protein coding sequence, SEQ ID 425.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 8; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 141
ID ABZ71421 standard; cDNA; 1050 BP.
DE Secreted protein-encoding gene 84 cDNA clone HKGDL36, SEQ ID NO:242.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 8; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 142
ID ADB91374 standard; cDNA; 1050 BP.
DE Human secreted protein cDNA #SEQ ID 320.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 9; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 143
ID ADC73869 standard; DNA; 1050 BP.
DE Human secreted protein-related DNA - SEQ ID 502.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 9; Length 1050;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 144
ID ACC50491 standard; cDNA; 1052 BP.
DE Human secreted protein coding sequence, SEQ ID 158.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 8; Length 1052;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 145
ID ABZ71273 standard; cDNA; 1052 BP.
DE Human secreted protein-encoding gene 84 cDNA clone HKGDL36, SEQ ID NO:94.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 8; Length 1052;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 146
ID ADB91179 standard; cDNA; 1052 BP.
DE Human secreted protein cDNA #SEQ ID 125.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 9; Length 1052;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 147
ID ADC73556 standard; DNA; 1052 BP.
DE Human secreted protein-related DNA - SEQ ID 189.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 10; Length 1052;
Best Local Similarity 78.0%; Pred. No. 0.033;
RESULT 148

ID AAC79804 standard; cDNA; 1390 BP.
DE Human secreted protein gene 6 SEQ ID NO:16.
PN WO200058336-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 3; Length 1390;
Best Local Similarity 78.0%; Pred. No. 0.034;
RESULT 149
ID ABI90541 standard; cDNA; 1857 BP.
DE Human polynucleotide SEQ ID NO 1103.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 64.8; DB 6; Length 1857;
Best Local Similarity 78.0%; Pred. No. 0.035;
RESULT 150
ID ACN46220 standard; cDNA; 121 BP.
DE Cotton primed seed EST clone ID: LIB3825-016-Q1-K6-H3, SEQ:1001.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.3%; Score 64.6; DB 13; Length 121;
Best Local Similarity 70.4%; Pred. No. 0.032;
RESULT 151
ID ABR97599 standard; cDNA; 503 BP.
DE Human prostate specific nucleic acid DEX0293_26.
PN WO200255735-A2.
PD 18-JUL-2002.
PA (DIAD-) DIADENUS INC.
Query Match 11.3%; Score 64.6; DB 6; Length 503;
Best Local Similarity 65.7%; Pred. No. 0.034;
RESULT 152
ID ADI27232 standard; DNA; 1718 BP.
DE Rat LRP binding family associated DNA.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 11.3%; Score 64.6; DB 12; Length 1718;
Best Local Similarity 80.0%; Pred. No. 0.037;
RESULT 153
ID ADI27111 standard; DNA; 1718 BP.
DE Rat LRP binding family protein DNA #2.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 11.3%; Score 64.6; DB 12; Length 1718;
Best Local Similarity 80.0%; Pred. No. 0.037;
RESULT 154
ID AAH33160 standard; cDNA; 253 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:216.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 64.4; DB 4; Length 253;
Best Local Similarity 71.6%; Pred. No. 0.036;
RESULT 155
ID ACC68993 standard; cDNA; 811 BP.
DE Human neurotransmission-associated protein NTRAN-15 cDNA SEQ ID NO:40.
PN WO2003025129-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.3%; Score 64.4; DB 10; Length 811;
Best Local Similarity 70.5%; Pred. No. 0.038;
RESULT 156
ID AAC98220 standard; cDNA; 1798 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:230.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 64.4; DB 3; Length 1798;

Best Local Similarity 71.6%; Pred. No. 0.04;
RESULT 157
ID AAL16089 standard; cDNA; 495 BP.
DE Human breast cancer expressed polynucleotide 8546.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.3%; Score 64.2; DB 4; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.04;
RESULT 158
ID ACN47369 standard; cDNA; 539 BP.
DE Cotton primed seed EST Clone ID: LIB3825-010-Q1-N6-F2, SEQ:2150.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.3%; Score 64.2; DB 13; Length 539;
Best Local Similarity 71.8%; Pred. No. 0.041;
RESULT 159
ID ACN45362 standard; cDNA; 570 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.3%; Score 64.2; DB 13; Length 570;
Best Local Similarity 77.2%; Pred. No. 0.041;
RESULT 160
ID ACN6045 standard; DNA; 849 BP.
DE Breast cancer related marker, seq id 7195.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 64.2; DB 11; Length 849;
Best Local Similarity 66.7%; Pred. No. 0.042;
RESULT 161
ID ACA92436 standard; DNA; 1647 BP.
DE DNA encoding human PMW-21.
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.3%; Score 64.2; DB 10; Length 1647;
Best Local Similarity 89.6%; Pred. No. 0.043;
RESULT 162
ID AAI90382 standard; cDNA; 440 BP.
DE Human polynucleotide SEQ ID NO 10442.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSE INC.
Query Match 11.2%; Score 64; DB 4; Length 440;
Best Local Similarity 78.5%; Pred. No. 0.043;
RESULT 163
ID ABO54884 standard; cDNA; 1339 BP.
DE Human ovarian antigen HaOS253 cDNA, SEQ ID NO:764.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 11.2%; Score 64; DB 6; Length 1339;
Best Local Similarity 73.2%; Pred. No. 0.046;
RESULT 164
ID ADP65758 standard; DNA; 1451 BP.
DE Human Tax interaction protein 1 (TIP-1) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 11.2%; Score 64; DB 11; Length 1451;
Best Local Similarity 73.2%; Pred. No. 0.047;
RESULT 165
ID ADP65836 standard; DNA; 1451 BP.
PD 29-MAY-2003.

DE Human Tax interaction protein 1 mRNA, complete cds DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 11.2%; Score 64; DB 11; Length 1451;
Best Local Similarity 73.2%; Pred. No. 0.047;
RESULT 166
ID ADP24212 standard; cDNA; 1451 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1390.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GSTH-) GENENTECH INC.
Query Match 11.2%; Score 64; DB 13; Length 1451;
Best Local Similarity 73.2%; Pred. No. 0.047;
RESULT 167
ID ACN5513 standard; cDNA; 235 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-029-Q6-K6-H3, SEQ:9916.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.2%; Score 63.8; DB 13; Length 235;
Best Local Similarity 55.9%; Pred. No. 0.045;
RESULT 168
ID ABV83658 standard; cDNA; 254 BP.
DE Human breast specific gene SEQ ID NO 101.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADENUS INC.
Query Match 11.2%; Score 63.8; DB 6; Length 254;
Best Local Similarity 67.9%; Pred. No. 0.045;
RESULT 169
ID AAK5675 standard; cDNA; 893 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:1635.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 11.2%; Score 63.8; DB 4; Length 893;
Best Local Similarity 85.5%; Pred. No. 0.049;
RESULT 170
ID AA206222 standard; DNA; 1621 BP.
DE Human secreted protein gene No. 4.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 11.2%; Score 63.8; DB 2; Length 1621;
Best Local Similarity 90.7%; Pred. No. 0.051;
RESULT 171
ID AAL16186 standard; cDNA; 449 BP.
DE Human breast cancer expressed polynucleotide 8643.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.2%; Score 63.6; DB 4; Length 449;
Best Local Similarity 63.4%; Pred. No. 0.051;
RESULT 172
ID ACN49090 standard; cDNA; 506 BP.
DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-N6-A2, SEQ:3871.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 11.2%; Score 63.6; DB 13; Length 506;
Best Local Similarity 73.6%; Pred. No. 0.051;
RESULT 173
ID ACN6134 standard; DNA; 1023 BP.
DE Breast cancer related marker, seq id 7284.
PN US2003099974-A1.
PD 29-MAY-2003.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 63.6; DB 11; Length 1023;
Best Local Similarity 63.4%; Pred. No. 0.053;
RESULT 174
ID AAV63176 standard; cDNA, 1307 BP.
DE cDNA from clone dxk279_1 which encodes a secreted protein.
PN WO9840486-A2.
PD 17-SEP-1998.
PA (GEMV) GENETICS INST. INC.
Query Match 11.2%; Score 63.6; DB 2; Length 1307;
Best Local Similarity 71.2%; Pred. No. 0.054;
RESULT 175
ID AAA00681 standard; cDNA, 251 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:672.
PN WO958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
Query Match 11.1%; Score 63.4; DB 3; Length 251;
Best Local Similarity 74.5%; Pred. No. 0.053;
RESULT 176
ID ABL87269 standard; cDNA, 451 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10247.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 11.1%; Score 63.4; DB 6; Length 451;
Best Local Similarity 70.2%; Pred. No. 0.055;
RESULT 177
ID AAC79968 standard; cDNA, 815 BP.
DE Human secreted protein encoding cDNA for gene 21.
PN WO200058357-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 63.4; DB 3; Length 815;
Best Local Similarity 78.4%; Pred. No. 0.057;
RESULT 178
ID AAC79692 standard; cDNA, 1662 BP.
DE Human ORFX ORF2547 polynucleotide sequence SEQ ID NO:5093.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 11.1%; Score 63.4; DB 3; Length 1662;
Best Local Similarity 70.2%; Pred. No. 0.06;
RESULT 179
ID ABQ74268 standard; cDNA, 6582 BP.
DE Human 67076 transporter protein encoding cDNA SEQ ID NO:13.
PN WO200255701-A2.
PD 18-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.1%; Score 63.4; DB 6; Length 6582;
Best Local Similarity 91.8%; Pred. No. 0.065;
RESULT 180
ID ADD37486 standard; cDNA, 6582 BP.
DE Human transporter 67076 cDNA #1.
PN US2003143675-A1.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.1%; Score 63.4; DB 10; Length 6582;
Best Local Similarity 91.8%; Pred. No. 0.065;
RESULT 181
ID ADI27965 standard; cDNA, 6582 BP.
DE Human 67076 cDNA.
PN US2003155891-A1.
PD 04-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.1%; Score 63.4; DB 12; Length 6582;
Best Local Similarity 91.8%; Pred. No. 0.065;
RESULT 182
ID ABX42770 standard; cDNA, 212 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7935.
PN US2002137139-A1.
PD 26-SEP-2002.

PA (BYAT/) BYATT J. C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W. C.
Query Match 11.1%; Score 63.2; DB 8; Length 212;
Best Local Similarity 74.1%; Pred. No. 0.057;
RESULT 183
ID AAI90374 standard; cDNA, 429 BP.
DE Human polynucleotide SEQ ID NO:10434.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.1%; Score 63.2; DB 4; Length 429;
Best Local Similarity 84.5%; Pred. No. 0.059;
RESULT 184
ID ACH21618 standard; cDNA, 430 BP.
DE Human adult liver cDNA #1230.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R. T.
PA (LABA/) LABAT I. C.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M. C.
PA (JONE/) JONES L. W.
Query Match 11.1%; Score 63.2; DB 9; Length 430;
Best Local Similarity 71.6%; Pred. No. 0.059;
RESULT 185
ID AAI84683 standard; cDNA, 437 BP.
DE Human polynucleotide SEQ ID NO:4743.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.1%; Score 63.2; DB 4; Length 437;
Best Local Similarity 84.5%; Pred. No. 0.059;
RESULT 186
ID ABV55470 standard; cDNA, 474 BP.
DE Human prostate expression marker cDNA 55461.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.1%; Score 63.2; DB 5; Length 474;
Best Local Similarity 84.5%; Pred. No. 0.06;
RESULT 187
ID ACN52740 standard; cDNA, 580 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-H12, SEQ:7521.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (PENG/) PENG P. C. C.
PA (FINC/) FINCHER K. L.
PA (ZIEG/) ZIEGLER T. E.
Query Match 11.1%; Score 63.2; DB 13; Length 580;
Best Local Similarity 77.0%; Pred. No. 0.061;
RESULT 188
ID AAI19087 standard; cDNA, 598 BP.
DE Human breast cancer expressed polynucleotide 11544.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.1%; Score 63.2; DB 4; Length 598;
Best Local Similarity 71.6%; Pred. No. 0.061;
RESULT 189
ID AAF21763 standard; cDNA, 780 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 150.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 63.2; DB 3; Length 780;
Best Local Similarity 84.5%; Pred. No. 0.062;
RESULT 190
ID ADS73173 standard; cDNA, 882 BP.
DE Human kidney tumour specific cDNA, SEQ ID 1770.
PN US2003109434-A1.

PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 11.1%; Score 63.2; DB 7; Length 882;
RESULT 191
ID ADQ24215 standard; DNA; 1469 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7035.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 11.1%; Score 63.2; DB 12; Length 1469;
RESULT 192
ID ABT08077 standard; cDNA; 2365 BP.
DE Human breast specific coding sequence SEQ ID NO: 23.
PN WO200266607-A2.
PD 23-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 11.1%; Score 63.2; DB 6; Length 2365;
RESULT 193
ID ABV57207 standard; cDNA; 394 BP.
DE Human prostate expression marker cDNA 57198.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 11.1%; Score 63; DB 5; Length 394;
RESULT 194
ID AAD02077 standard; cDNA; 396 BP.
DE cDNA encoding rat pituitary hormone, pituitrone.
PN WO200066778-A1.
PD 09-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.1%; Score 63; DB 3; Length 396;
RESULT 195
ID ABV54374 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 54365.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 11.1%; Score 63; DB 5; Length 407;
RESULT 196
ID AA184858 standard; cDNA; 451 BP.
DE Human polynucleotide SEQ ID NO 4918.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.1%; Score 63; DB 4; Length 451;
RESULT 197
ID ADQ24028 standard; DNA; 747 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6848.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 11.1%; Score 63; DB 12; Length 747;
RESULT 198
ID ADM03187 standard; cDNA; 2335 BP.
DE Human cDNA of the invention SEQ ID NO:1872.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 11.1%; Score 63; DB 11; Length 2335;
RESULT 199
ID ABX71310 standard; cDNA; 2042 BP.
DE Human transmembrane protein cDNA clone DKFZphutcl_19f19.
PN WO200112659-A2.
PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match
Best Local Similarity 11.0%; Score 62.8; DB 5; Length 2042;
RESULT 200
ID ABK43731 standard; cDNA; 2292 BP.
DE DNA encoding novel central nervous system protein #311.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 62.8; DB 4; Length 2292;
RESULT 201
ID AD154118 standard; cDNA; 2292 BP.
DE cDNA encoding novel human protein seq id 321.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 11.0%; Score 62.8; DB 12; Length 2292;
RESULT 202
ID ADO23054 standard; DNA; 3650 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5874.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 11.0%; Score 62.8; DB 12; Length 3650;
RESULT 203
ID ABV58264 standard; cDNA; 201 BP.
DE Human prostate expression marker cDNA 58255.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 5; Length 201;
RESULT 204
ID ABV60873 standard; cDNA; 338 BP.
DE Human prostate expression marker cDNA 60864.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 5; Length 338;
RESULT 205
ID AA183450 standard; cDNA; 365 BP.
DE Human polynucleotide SEQ ID NO 3510.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 4; Length 365;
RESULT 206
ID AAC78443 standard; cDNA; 386 BP.
DE Human cancer associated gene sequence SEQ ID NO:837.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 3; Length 386;
RESULT 207
ID AA191255 standard; cDNA; 388 BP.
DE Human polynucleotide SEQ ID NO 11315.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 4; Length 388;
RESULT 208
ID AA183044 standard; cDNA; 424 BP.
DE Human polynucleotide SEQ ID NO 3104.
PN WO200164835-A2.

PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.0%; Score 62.6; DB 4; Length 424;
Best Local Similarity 88.3%; Pred. No. 0.075;
RESULT 209
ID ADG3117 standard; DNA; 508 BP.
DE Human DNA differentially expressed in patients with SLE SeqID441.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 11.0%; Score 62.6; DB 10; Length 508;
Best Local Similarity 70.9%; Pred. No. 0.076;
RESULT 210
ID AAD56360 standard; DNA; 543 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HDWG72, SEQ ID NO:20.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 62.6; DB 9; Length 543;
Best Local Similarity 65.9%; Pred. No. 0.076;
RESULT 211
ID ACN46017 standard; cDNA; 543 BP.
DE Cccton primed seed EST Clone ID: LIB3825-013-Q1-N6-A6, SEQ:798.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIGC/) ZIGGLER T E.
Query Match 11.0%; Score 62.6; DB 13; Length 543;
Best Local Similarity 70.9%; Pred. No. 0.076;
RESULT 212
ID AAC80546 standard; cDNA; 587 BP.
DE Human secreted protein gene 16 SEQ ID NO:26.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 62.6; DB 3; Length 587;
Best Local Similarity 76.2%; Pred. No. 0.077;
RESULT 213
ID AAL20298 standard; cDNA; 610 BP.
DE Human breast cancer expressed polynucleotide 12755.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLERNIUM PREDICTIVE MEDICINE INC.
Query Match 11.0%; Score 62.6; DB 4; Length 610;
Best Local Similarity 70.9%; Pred. No. 0.077;
RESULT 214
ID AAL02545 standard; cDNA; 818 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2546.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 62.6; DB 4; Length 818;
Best Local Similarity 73.3%; Pred. No. 0.078;
RESULT 215
ID ADF81418 standard; DNA; 2311 BP.
DE Leukemia-related DNA sequence #1974.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HARE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 11.0%; Score 62.6; DB 10; Length 2311;
Best Local Similarity 59.1%; Pred. No. 0.083;
RESULT 216
ID ACN40655 standard; cDNA; 2311 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326739, SEQ ID NO:5566.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 11.0%; Score 62.6; DB 13; Length 2311;
Best Local Similarity 59.1%; Pred. No. 0.083;
RESULT 217
ID AAT61590 standard; cDNA; 2589 BP.
DE Human C-ITAP1.
PN WO9706192-A1.
PD 20-FEB-1997.
PA (TULA-) TULARIK INC.
Query Match 11.0%; Score 62.6; DB 2; Length 2589;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 218
ID ADR89078 standard; DNA; 2589 BP.
DE IAP cleaving polypeptide encoding DNA.
PN WO2004072241-A2.
PD 26-AUG-2004.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 11.0%; Score 62.6; DB 13; Length 2589;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 219
ID ADR89077 standard; DNA; 2589 BP.
DE IAP cleaving polypeptide encoding DNA.
PN WO2004072241-A2.
PD 26-AUG-2004.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 11.0%; Score 62.6; DB 13; Length 2589;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 220
ID AAS08630 standard; cDNA; 2732 BP.
DE Human cDNA (DNA148380-2827) encoding a Stra6 homologue, PRO10282.
PN WO200151635-A2.
PD 19-JUL-2001.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 4; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 221
ID ABR33575 standard; cDNA; 2732 BP.
DE cDNA encoding human PRO protein, Seq ID No 79.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 6; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 222
ID ABR47278 standard; cDNA; 2732 BP.
DE cDNA encoding human Stra6 (PRO10282) protein.
PN WO200218608-A2.
PD 07-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 6; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 223
ID ACA68536 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 8; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 224
ID ABR44265 standard; cDNA; 2732 BP.
DE Human PRO10282 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 225
ID ABR44548 standard; cDNA; 2732 BP.
DE Human PRO10282 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;

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Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 226
ID ACD82215 standard; cDNA; 2732 BP.
DE Human secreted/transmembrane polypeptide PRO 10282 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 227
ID AB743921 standard; cDNA; 2732 BP.
DE Human membrane bound receptor/protein PRO10282 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 228
ID ADB83569 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 229
ID ADB80675 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003080658-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 230
ID ADB73216 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096568-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 231
ID ADB78298 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 232
ID ADB84946 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 233
ID ADB78052 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 234
ID ADB87118 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 235
ID ADB84700 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 236
ID ADB83815 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 237
ID ADB72970 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 238
ID ADC36808 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US200308065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 239
ID ADC21798 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 240
ID ADC49829 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US200308064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 241
ID ADC49028 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US200308070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 242
ID ADC49545 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US200308071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 243
ID ADC47406 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US200308072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 244
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ID ADC47151 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 245
ID ADC78026 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 246
ID ADD06261 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 247
ID ADC77780 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 248
ID ADD50743 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 249
ID ADD50989 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 250
ID ADD50470 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 251
ID ADD50224 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 252
ID ADD51235 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 253
ID ACA66880 standard; cDNA; 2732 BP.

DE cDNA encoding human PRO polypeptide #40.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 254
ID ACD68632 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 255
ID ADC48782 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 256
ID ADE20953 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 257
ID ADE05797 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 258
ID ADD75026 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 259
ID ADD75772 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 260
ID ADD85004 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 261
ID ADD86830 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 262
ID ADE20707 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.

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PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 263
ID ADE39004 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 264
ID ADE05551 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 265
ID ADD73536 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 266
ID ADD78376 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 267
ID ADE21199 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 268
ID ADD77314 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 269
ID ADE20461 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 270
ID ADD75526 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 271
ID ADD74042 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 272
ID ADD74288 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 273
ID ADD76018 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 274
ID ADE85510 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 275
ID ADE05059 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 276
ID ADD75272 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 277
ID ADD76816 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 278
ID ADE6584 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 279
ID ADD78052 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 280
ID ADD77560 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 281
ID ADD77806 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 282
ID ADD85264 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 283
ID ADD73796 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 284
ID ADD74534 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 285
ID ADD77062 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 286
ID ADD85756 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 287
ID ADE05305 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 288
ID ADD74780 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 289
ID ADG05592 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 290
ID ADG27146 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 291
ID ADG11209 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 292
ID ADG11988 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 293
ID ADP94545 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 294
ID ADG06641 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 295
ID ADH3985 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 296
ID ADG34075 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 297
ID ADI33545 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 298
ID ADH69639 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;

Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 299
ID AD129800 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 300
ID ADM27197 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 301
ID ADK6655 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 302
ID ADO24087 standard; DNA; 2929 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6907.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.0%; Score 62.6; DB 12; Length 2929;
Best Local Similarity 88.3%; Pred. No. 0.085;
RESULT 303
ID ADO22314 standard; DNA; 3058 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5134.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.0%; Score 62.6; DB 12; Length 3058;
Best Local Similarity 83.5%; Pred. No. 0.085;
RESULT 304
ID ABS54600 standard; cDNA; 3082 BP.
DE cDNA encoding human Ras-like protein.
PN WO200262849-A2.
PD 15-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 11.0%; Score 62.6; DB 6; Length 3082;
Best Local Similarity 83.5%; Pred. No. 0.085;
RESULT 305
ID ABV54585 standard; cDNA; 257 BP.
DE Human prostate expression marker cDNA 54576.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.4; DB 5; Length 257;
Best Local Similarity 90.4%; Pred. No. 0.079;
RESULT 306
ID ABV58905 standard; cDNA; 337 BP.
DE Human prostate expression marker cDNA 58896.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.4; DB 5; Length 337;
Best Local Similarity 81.8%; Pred. No. 0.08;
RESULT 307
ID ACN87128 standard; DNA; 363 BP.
DE Breast cancer related marker, seq id 8278.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.9%; Score 62.4; DB 11; Length 363;
Best Local Similarity 69.2%; Pred. No. 0.081;

RESULT 308
ID AAL25958 standard; cDNA; 422 BP.
DE Human breast cancer expressed polynucleotide 18415.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.4; DB 4; Length 422;
Best Local Similarity 86.2%; Pred. No. 0.081;
RESULT 309
ID ACN88851 standard; DNA; 422 BP.
DE Breast cancer related marker, seq id 10001.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.9%; Score 62.4; DB 11; Length 422;
Best Local Similarity 86.2%; Pred. No. 0.081;
RESULT 310
ID ACH4551 standard; cDNA; 445 BP.
DE Human foetal brain cDNA #6276.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.9%; Score 62.4; DB 9; Length 445;
Best Local Similarity 75.0%; Pred. No. 0.082;
RESULT 311
ID AAL19123 standard; cDNA; 466 BP.
DE Human breast cancer expressed polynucleotide 11580.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.4; DB 4; Length 466;
Best Local Similarity 86.2%; Pred. No. 0.082;
RESULT 312
ID ACN55464 standard; cDNA; 540 BP.
DE Cotton androscium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.9%; Score 62.4; DB 13; Length 540;
Best Local Similarity 81.8%; Pred. No. 0.083;
RESULT 313
ID ACN45417 standard; cDNA; 565 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-G5, SEQ:198.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.9%; Score 62.4; DB 13; Length 565;
Best Local Similarity 81.8%; Pred. No. 0.083;
RESULT 314
ID ABQ7535 standard; cDNA; 626 BP.
DE Human lung specific nucleic acid sequence SEQ ID NO:94.
PN WO200264788-A2.
PD 22-AUG-2002.
PA (DIAD-) DIADKUS INC.
Query Match 10.9%; Score 62.4; DB 6; Length 626;
Best Local Similarity 81.8%; Pred. No. 0.083;
RESULT 315
ID AAA26286 standard; cDNA; 2608 BP.
DE Human secreted protein gene 6 SEQ ID NO:16.
PN WO200011014-A1.
PD 02-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 62.4; DB 3; Length 2608;

Best Local Similarity 86.2%; Pred. No. 0.091;
RESULT 316
ID AAF60867 standard; cDNA; 5714 BP.
DE Human TAA R11 cDNA.
PN DE19936563-A1.
PD 08-FEB-2001.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 10.9%; Score 62.4; DB 4; Length 5714;
Best Local Similarity 98.4%; Pred. No. 0.095;
RESULT 317
ID ABL3126 standard; DNA; 6338 BP.
DE Human immune system associated gene SEQ ID NO: 1099.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPICGENOMICS AG.
Query Match 10.9%; Score 62.4; DB 6; Length 6338;
Best Local Similarity 70.0%; Pred. No. 0.096;
RESULT 318
ID AAI87993 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 8053.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 62.2; DB 4; Length 416;
Best Local Similarity 84.3%; Pred. No. 0.088;
RESULT 319
ID ADI45027 standard; DNA; 448 BP.
DE Human ovarian cancer DNA marker #18917.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.2; DB 5; Length 448;
Best Local Similarity 61.3%; Pred. No. 0.088;
RESULT 320
ID ABV56397 standard; cDNA; 550 BP.
DE Human prostate expression marker cDNA 56388.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62.2; DB 5; Length 550;
Best Local Similarity 67.2%; Pred. No. 0.09;
RESULT 321
ID AAF15652 standard; cDNA; 597 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:87.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 10.9%; Score 62.2; DB 3; Length 597;
Best Local Similarity 87.0%; Pred. No. 0.09;
RESULT 322
ID AAF16238 standard; cDNA; 1430 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:673.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 10.9%; Score 62.2; DB 3; Length 1430;
Best Local Similarity 76.0%; Pred. No. 0.095;
RESULT 323
ID ABA93758 standard; cDNA; 1537 BP.
DE Human testis derived cDNA clone test3_22124.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GERH-) GERMAN HUMAN GENOME PROJECT.
Query Match 10.9%; Score 62.2; DB 6; Length 1537;
Best Local Similarity 89.3%; Pred. No. 0.095;
RESULT 324
ID AAF97884 standard; cDNA; 2329 BP.
DE Human secreted protein cDNA, SEQ ID NO: 11.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.9%; Score 62.2; DB 4; Length 2329;
Best Local Similarity 89.3%; Pred. No. 0.098;
RESULT 325
ID AAV40745 standard; cDNA; 2836 BP.
DE C. felis esterase, nFE72836, coding sequence complementary strand.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match 10.9%; Score 62.2; DB 2; Length 2836;
Best Local Similarity 89.3%; Pred. No. 0.099;
RESULT 326
ID AAV40744 standard; cDNA; 2836 BP.
DE C. felis esterase, nFE72836, coding sequence.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match 10.9%; Score 62.2; DB 2; Length 2836;
Best Local Similarity 89.3%; Pred. No. 0.099;
RESULT 327
ID AAD21170 standard; cDNA; 2836 BP.
DE Ctenocephalides felis carboxylesterase full length cDNA, nFE72836.
PN US6291222-B1.
PD 18-SEP-2001.
PA (HESK-) HESKA CORP.
Query Match 10.9%; Score 62.2; DB 4; Length 2836;
Best Local Similarity 89.3%; Pred. No. 0.099;
RESULT 328
ID ABL35416 standard; DNA; 6265 BP.
DE Human immune system associated gene SEQ ID NO: 1389.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPICGENOMICS AG.
Query Match 10.9%; Score 62.2; DB 6; Length 6265;
Best Local Similarity 76.8%; Pred. No. 0.1;
RESULT 329
ID ABV57838 standard; cDNA; 216 BP.
DE Human prostate expression marker cDNA 57829.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62; DB 5; Length 216;
Best Local Similarity 72.7%; Pred. No. 0.092;
RESULT 330
ID ABV60981 standard; cDNA; 360 BP.
DE Human prostate expression marker cDNA 60972.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.9%; Score 62; DB 5; Length 360;
Best Local Similarity 70.3%; Pred. No. 0.095;
RESULT 331
ID ABX45485 standard; cDNA; 418 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10650.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 10.9%; Score 62; DB 8; Length 418;
Best Local Similarity 87.2%; Pred. No. 0.095;
RESULT 332
ID ACN58594 standard; cDNA; 486 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-010-06-N6-A7, SEQ:13375.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (PING/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.9%; Score 62; DB 13; Length 486;
Best Local Similarity 82.6%; Pred. No. 0.096;
RESULT 333

ID AA27250 standard; cDNA; 985 BP.
DE Human secreted protein cDNA encoding gene 18.
PN MO9946289-A1.
PD 16-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 62; DB 2; Length 985;
Best Local Similarity 82.6%; Pred. No. 0.1;
RESULT 334
ID AAD29756 standard; DNA; 3459 BP.
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.
PN WO200202630-A2.
PD 10-JUN-2002.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 10.9%; Score 62; DB 6; Length 3459;
Best Local Similarity 70.3%; Pred. No. 0.11;
RESULT 335
ID AA18481 standard; cDNA; 388 BP.
DE Human polynucleotide SEQ ID NO 4871.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 61.8; DB 4; Length 388;
Best Local Similarity 74.3%; Pred. No. 0.1;
RESULT 336
ID ACH36139 standard; cDNA; 508 BP.
DE Human endothelial cell cDNA #4272.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA-) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.8%; Score 61.8; DB 9; Length 508;
Best Local Similarity 90.4%; Pred. No. 0.1;
RESULT 337
ID ABV58598 standard; cDNA; 608 BP.
DE Human prostate expression marker cDNA 58589.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.8; DB 5; Length 608;
Best Local Similarity 90.4%; Pred. No. 0.11;
RESULT 338
ID AD162858 standard; cDNA; 739 BP.
DE Human apoptosis-associated cDNA SEQ ID 301.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 10.8%; Score 61.8; DB 10; Length 739;
Best Local Similarity 53.5%; Pred. No. 0.11;
RESULT 339
ID AD162891 standard; cDNA; 739 BP.
DE Human apoptosis-associated cDNA SEQ ID 334.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 10.8%; Score 61.8; DB 10; Length 739;
Best Local Similarity 53.5%; Pred. No. 0.11;
RESULT 340
ID AD162874 standard; cDNA; 739 BP.
DE Human apoptosis-associated cDNA SEQ ID 317.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 10.8%; Score 61.8; DB 10; Length 739;
Best Local Similarity 53.5%; Pred. No. 0.11;
RESULT 341
ID AA194904 standard; cDNA; 754 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 979.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.

PA (HISM-) HISAMITSU PHARM CO LTD.
Query Match 10.8%; Score 61.8; DB 4; Length 754;
Best Local Similarity 78.4%; Pred. No. 0.11;
RESULT 342
ID ABS57568 standard; cDNA; 1370 BP.
DE Human SECP-24 cDNA from clone 7503458CD1 SEQ ID 24.
PN WO200279441-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1370;
Best Local Similarity 77.3%; Pred. No. 0.11;
RESULT 343
ID AA16659 standard; cDNA; 1476 BP.
DE Human secreted protein clone y690_1 nucleotide sequence SEQ ID NO:83.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY-) GENNETICS INST INC.
Query Match 10.8%; Score 61.8; DB 3; Length 1476;
Best Local Similarity 85.2%; Pred. No. 0.11;
RESULT 344
ID AA265060 standard; cDNA; 1483 BP.
DE Membrane-bound protein PRO1105 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 3; Length 1483;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 345
ID AAS46034 standard; cDNA; 1484 BP.
DE Human DNA encoding PRO polypeptide sequence #110.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 4; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 346
ID AAP44206 standard; cDNA; 1484 BP.
DE Human PRO1105 (UNQ548) nucleotide sequence SEQ ID NO:292.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 5; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 347
ID ACA89484 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 348
ID ACA73494 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 349
ID ACA05809 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 350
ID ACA66643 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO protein #110.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 351
ID ACFA64353 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 352
ID ACFF20218 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 353
ID ACFF19604 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 354
ID ACD21892 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 355
ID ACFF13057 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 356
ID ACD25160 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 357
ID ACF00209 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 358
ID ACA72266 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 359
ID ACD04790 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 360
ID ACD18251 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 361
ID ACD08258 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 362
ID ACBA8692 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 363
ID ACA70134 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 364
ID ACD12356 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 365
ID ACCT4271 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 366
ID ACD15899 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 367
ID ACD25467 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 368
ID ACD17944 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 369
ID ACC88231 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 370
ID ACD21585 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 371
ID ACD18652 standard; cDNA; 1484 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 372
ID ABX98262 standard; cDNA; 1484 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID NO:219.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 373
ID ACD14013 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 374
ID ACD09793 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 375
ID ACC88538 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 376
ID ACD21278 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 377
ID ABX75650 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1105.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 378
ID ABX97853 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 379
ID ACA97329 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 380
ID ACA57792 standard; cDNA; 1484 BP.
DE Human PRO1105 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 381
ID ACD14320 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032130-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 382
ID ACC91103 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 383
ID ACC8845 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 384
ID ACD07042 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 385
ID ACA67493 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 386
ID ACC81548 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 387
ID ACC89152 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 388
ID ACC86508 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 389
ID ACC89766 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 390
ID ACC92945 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
PRED. NO. 0.11;
RESULT 391
ID ABX80812 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein cDNA, #120.
PN US2003027162-A1.

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PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 392
ID ACA72573 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 393
ID ACA83091 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 394
ID ACA69827 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 395
ID ACA96970 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 396
ID ACA90966 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 397
ID ACA70748 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 398
ID ACA95258 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 399
ID ACDA4321 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 400
ID ACC86201 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 401
ID ACC90073 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 402
ID ACD1681 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 403
ID ACF1911 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 404
ID ABX76855 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 405
ID ACA73187 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 406
ID ACA68730 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 407
ID ACA74574 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 408
ID ACA70441 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 409
ID ACD14627 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 410
ID ACA68299 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 411
ID ABX98764 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 412
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ID ACC81241 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 413
ID ACA95565 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 414
ID ACD04483 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 415
ID ACC87924 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 416
ID ACB12586 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 417
ID ABX79492 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein cDNA, #120.
PN US2002142861-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 418
ID ACA96301 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 419
ID ACA65075 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 420
ID ACA73801 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 421
ID ACA74213 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 422
ID ACA96608 standard; cDNA; 1484 BP.

DE Human PRO polynucleotide #110.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 423
ID ACD10714 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 424
ID ACC91410 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 425
ID ACA93513 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 426
ID ACD02745 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 427
ID ACC87310 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 428
ID ACC85894 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 429
ID ABX81195 standard; DNA; 1484 BP.
DE Novel human secreted or transmembrane protein PRO511 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 430
ID ACA65382 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 431
ID ACA94199 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;
67.4%; Pred. No. 0.11;
RESULT 432
ID ACA97943 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003036145-A1.

PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 433
ID ACA91445 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 434
ID ACA9659 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 435
ID ACD16206 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 436
ID ACD17367 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 437
ID ACC92024 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 438
ID ACA74881 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 439
ID ACA91752 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 440
ID ACA71396 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 441
ID ACC90796 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 442
ID ACA65806 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO protein #110.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 443
ID ACA93011 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 444
ID ACA94951 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 445
ID ACD16513 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 446
ID ACD1592 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 447
ID ABX17095 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2002123463-A1.
PD 05-SEP-2002.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 448
ID ABX16695 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein #110.
PN US2002127584-A1.
PD 12-SEP-2002.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 449
ID ACA67950 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
Query Match 10.8%; Score 61.8; DB 8; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 450
ID ACA97636 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 451
ID ACA99085 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 452
ID ACC91717 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040076-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 453
ID ACD1128 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 454
ID ACD14978 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 455
ID ACA88399 standard; cDNA; 1484 BP.
DE Human secreted and transmembrane polypeptide PRO1105 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 456
ID ACD81906 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 457
ID ACD11742 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 458
ID ACC95871 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 459
ID ACF16434 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 460
ID ACF02552 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 461
ID ACF02859 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 462
ID ACF21446 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049769-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 463
ID ACF10130 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 464
ID ACF78023 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 465
ID ACD46728 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 466
ID ACD49491 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 467
ID ACF28258 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 468
ID ACD88948 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 469
ID ACD84343 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 470
ID ACD99117 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 471
ID ADA77971 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003073180-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 472
ID ACF4859 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 473
ID ACD09179 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036131-A1.
PD 20-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 474
ID ACF11972 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 475
ID ACF41206 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 476
ID ACF15820 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 477
ID ACF16127 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 478
ID ACD31954 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 479
ID ACF18762 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 480
ID ACF09209 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 481
ID ACF78330 standard; cDNA; 1484 BP.

DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 482
ID ACF51929 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 483
ID ACF25416 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 484
ID ACF24209 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 485
ID ACF63520 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 486
ID ACF50394 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 487
ID ACH07865 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 488
ID ACF13671 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 489
ID ACD41597 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 490
ID ADA37803 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003008297-A1.

PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 491
ID ACF32010 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 492
ID ACF23288 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 493
ID ACF39978 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 494
ID ACF45500 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 495
ID ACF53157 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 496
ID ACF27337 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 497
ID ACF45175 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 498
ID ACF29793 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 499
ID ACD89869 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068695-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 500
ID ACD84650 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 501
ID ACD98810 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 502
ID ACF77102 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 503
ID ACF76795 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 504
ID ACF49780 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 505
ID ACF50087 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 506
ID ADA21489 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1105.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 507
ID ACD09486 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 508
ID ACD08565 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 509
ID ACF12279 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036130-A1.

ID 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 510
ID ACC94787 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 511
ID ACD22506 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 512
ID ACF15206 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 513
ID ACF97301 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 514
ID ACC92331 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 515
ID ACF13978 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 516
ID ACF14285 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 517
ID ADA10276 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1105.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 518
ID ACF09516 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 519

ID ACD45807 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 520
ID ACD47956 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 521
ID ACD67687 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 522
ID ACF25495 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 523
ID ACF29179 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 524
ID ACD84957 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 525
ID ACD84036 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 526
ID ACD86027 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 527
ID ACF30714 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 528
ID ACF32317 standard; cDNA; 1484 BP.

DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 529
ID ACHI1977 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 530
ID ACHI2284 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 531
ID ACDA0676 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 532
ID ADA17820 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 533
ID ACF18148 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 534
ID ACF08595 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 535
ID ACF31396 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 536
ID ACF52236 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 537
ID ACDS0105 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 540
ID ACF24823 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 541
ID ACF46403 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 542
ID ACF27951 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 543
ID ACD89255 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 544
ID ACF63827 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 545
ID ACF60467 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 546
ID ACHI2591 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 547
ID ACHI0014 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 548
ID ACD03869 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 549
ID ACD10407 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 550
ID ACD12049 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 551
ID ACF42434 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 552
ID ADA27928 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 553
ID ACF18455 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059865-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 554
ID ACF02245 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 555
ID ACF21753 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 556
ID ACF10437 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073169-A1.

PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 557
ID ACF33889 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 558
ID ACF44851 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 559
ID ACD90483 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 560
ID ACD91096 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 561
ID ACF30407 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 562
ID ACD87106 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 563
ID ACF60160 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073165-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 564
ID ACF46710 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003067373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 565
ID ACF75567 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 566
ID ADA79763 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 567
ID ACF17227 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 568
ID ACF22981 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 569
ID ACF07981 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 570
ID ACF08288 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 571
ID ACF040592 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 572
ID ACF53771 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 573
ID ACD47035 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 574
ID ACF47938 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 575
ID ACF47324 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.

PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 576
ID ACF46096 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 577
ID ACD86185 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 578
ID ACF52543 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 579
ID ACF52850 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 580
ID ACF64843 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 581
ID ACF76488 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 582
ID ACF61388 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 583
ID ACF61695 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 584
ID ACD30726 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;

Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 585
ID ACD31647 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 586
ID ACD32568 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 587
ID ACF17534 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 588
ID ADA94508 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 589
ID ACF07367 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 590
ID ACF20525 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 591
ID ACF21139 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 592
ID ACF20832 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 593
ID ACD47649 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 594
ID ACF47631 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068736-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 595
ID ACF53464 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 596
ID ACD86799 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 597
ID ACH05047 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 598
ID ACF44544 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 599
ID ADA81490 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 600
ID ACD22199 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 601
ID ACD24546 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 602
ID ACD39749 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 603
ID ACD40056 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 623
ID ACH10321 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 624
ID ACF01324 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 625
ID ACF40899 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 626
ID ACD24239 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 627
ID ACD1340 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 628
ID ACF17841 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 629
ID ADA38733 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 630
ID ACF32624 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 631
ID ACF40285 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 632
ID ACF48245 standard; cDNA; 1484 BP.

DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 633
ID ACF38194 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 634
ID ACF25130 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 635
ID ACF27030 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 636
ID ACF29486 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 637
ID ACD87720 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 638
ID ACF76181 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 639
ID ACF49473 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 640
ID ACF43930 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GENTECH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 641
ID ACH06275 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GENTECH) GENENTECH INC.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 642
ID ACH05582 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 643
ID ADA83288 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 644
ID ACC92638 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 645
ID ACC93252 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 646
ID ACF19297 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 647
ID ACD12988 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 648
ID ACP06446 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 649
ID ACC94480 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 650
ID ACC97908 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044933-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 651
ID ACC94173 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003072710-A1.
PD 06-FEB-2003.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 652
ID ACF42127 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 653
ID ACD31033 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 654
ID ACD43062 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 655
ID ACD43369 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 656
ID ACF14899 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 657
ID ADA92854 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 658
ID ACF01631 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 659
ID ACF31703 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 660
ID ACD67380 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 661
ID ACD48570 standard; cDNA; 1484 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 662
ID ACD4877 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 663
ID ACF51315 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 664
ID ACF54078 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 665
ID ACF25802 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 666
ID ACF39115 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 667
ID ACF28872 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 668
ID ACD9789 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 669
ID ACD8492 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 670
ID ACH05354 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.

PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 671
ID ACF65150 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 672
ID ADB20331 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 673
ID ACF43623 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 674
ID ACH09093 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 675
ID ACH09400 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 676
ID ADA7583 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 677
ID ACF09823 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 678
ID ACF51008 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 679
ID ACF23902 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068763-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
PD 13-FEB-2003.
Query Match
RESULT 680
ID ACD88334 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US200306869-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 681
ID ACH09707 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 682
ID ACH10628 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 683
ID ACD11435 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 684
ID ACC96485 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 685
ID ACC98515 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 686
ID ACF41820 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 687
ID ACF16741 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 688
ID ACD32261 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 689
ID ACD30419 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.

PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 690
ID ACD41290 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 691
ID ACF07674 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 692
ID ACF31089 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 693
ID ACF77409 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 694
ID ACF11051 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 695
ID ACF32931 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 696
ID ACF26109 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 697
ID ACD83422 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;
RESULT 698
ID ACF23595 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 699
ID ACF43009 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 700
ID ACF4316 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 701
ID ACH05968 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 702
ID ACH08786 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 703
ID ACC90380 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 704
ID ACF10744 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 705
ID ACC93559 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 706
ID ACC96178 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 707
ID ACD24853 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 708
ID ACF01938 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.

PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 709
ID ACF22060 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 710
ID ACF22674 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 711
ID ACF08902 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 712
ID ACF33238 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 713
ID ACF54692 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 714
ID ACF48552 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 715
ID ACD47342 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 716
ID ACD49184 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 717
ID ACF37887 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068686-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 718
ID ACF30100 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 719
ID ACD87413 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 720
ID ACF62002 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 721
ID ACH10935 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 722
ID ACD10100 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 723
ID ACD16825 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 724
ID ACH65467 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 725
ID ACC99122 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 726
ID ACF00516 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 727
ID ACD40983 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.

PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 728
ID ACF14592 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 729
ID ACF22367 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 730
ID ACF78944 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 731
ID ACF11665 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 732
ID ADA22415 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1105.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 733
ID ACF51622 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 734
ID ACF33545 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 735
ID ACD49798 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 736
ID ACF37580 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068683-A1.
PD 10-APR-2003.

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Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 737
ID ACF28565 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 738
ID ACD88641 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 739
ID ACF75260 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 740
ID ACF61081 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 741
ID ACF44237 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 742
ID ACH08479 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 743
ID ACD39457 standard; cDNA; 1484 BP.
DE Human cDNA encoding PRO511.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 744
ID ACC3866 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 745
ID ACD20971 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 746
ID ACF06753 standard; cDNA; 1484 BP.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 747
ID ACD20664 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 748
ID ACD22813 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 749
ID ACF41513 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 750
ID ADA06581 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #90.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 751
ID ADA39274 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 752
ID ACF07060 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 753
ID ACF77716 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 754
ID ACD46114 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 755
ID ACF47017 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 756
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ID ACF54385 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 757
ID ACF45789 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 758
ID ACF45482 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 759
ID ACF38501 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 760
ID ACD89562 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 761
ID ACD85264 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 762
ID ACD8578 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 763
ID ACF75874 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 764
ID ACF60774 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 765
ID ACH05661 standard; cDNA; 1484 BP.

DE cDNA encoding human PRO polypeptide #110.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 766
ID ADA82654 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 767
ID ADB96300 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 768
ID ACF55920 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 769
ID ACF55306 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 770
ID ADB85962 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 771
ID ACF56227 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 772
ID ACF56534 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 773
ID ACF55613 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 774
ID ACF54999 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068771-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 775
ID ADC57772 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 776
ID ADC55136 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 777
ID ADC12003 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 778
ID ADC56425 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 779
ID ADC07480 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 780
ID ADC11470 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 781
ID ADC14592 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 782
ID ADD08124 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 783
ID ADC81949 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 784
ID ADD07591 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;

Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 785
ID ADC82482 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003059835-A1.
PD 27-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 786
ID ADD05692 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 787
ID ADD08662 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 788
ID ADD06911 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 789
ID ADC83158 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 790
ID ADD55265 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 791
ID ADD56223 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 792
ID ADD54661 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 793
ID ADE25815 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 794
ID ADD89050 standard; cDNA; 1484 BP.
DE Encoding sequence TAT253.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 795 67.4%; Pred. No. 0.11;
ID ADE26282 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 796 67.4%; Pred. No. 0.11;
ID ADF67219 standard; cDNA; 1484 BP.
DE Human PRO1105 nucleotide sequence SEQ ID NO:292.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 797 67.4%; Pred. No. 0.11;
ID ADG02687 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 798 67.4%; Pred. No. 0.11;
ID ADG01394 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 799 67.4%; Pred. No. 0.11;
ID ADP95569 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 800 67.4%; Pred. No. 0.11;
ID ADG12384 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 801 67.4%; Pred. No. 0.11;
ID ADH09044 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 802 67.4%; Pred. No. 0.11;
ID ADI35473 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 803 67.4%; Pred. No. 0.11;
ID ADH99965 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 804 67.4%; Pred. No. 0.11;
ID ABX78637 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 805 67.4%; Pred. No. 0.11;
ID ACA75609 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 806 67.4%; Pred. No. 0.11;
ID ACA71089 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 807 67.4%; Pred. No. 0.11;
ID ACC87617 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 808 67.4%; Pred. No. 0.11;
ID ACC87003 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 809 67.4%; Pred. No. 0.11;
ID ACD04176 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 810 67.4%; Pred. No. 0.11;
ID ABX77896 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 811 67.4%; Pred. No. 0.11;
ID ABX80308 standard; cDNA; 1484 BP.
DE Novel human secreted or transmembrane protein PRO511 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 812 67.4%; Pred. No. 0.11;
ID ACA69214 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 813 67.4%; Pred. No. 0.11;
ID ACA69507 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.8%; Score 61.8; DB 10; Length 1484;
RESULT 814 67.4%; Pred. No. 0.11;
ID ACA90352 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
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Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 815
ID ACC89459 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 816
ID ABX90285 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein cDNA, #120.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 817
ID ACA98250 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 818
ID ACA93892 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 819
ID ACD15285 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 820
ID ACD08872 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 821
ID ACC96792 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 822
ID ACF1513 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 823
ID ABX64131 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 824
ID ACA72880 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 825
ID ACD03052 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 826
ID ACD01867 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 827
ID ACA92059 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 828
ID ADL32825 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 11; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 829
ID ADM30359 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 11; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 830
ID ADE74356 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 831
ID ADE74968 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 832
ID ADF35418 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 833
ID ADG11668 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2003228653-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 834
ID ADF96181 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.

Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 835
ID ADG04452 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 836
ID ADG00612 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 837
ID ADG82868 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 838
ID ADH26149 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 839
ID ADH19538 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 840
ID ADH33118 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 841
ID ADH21031 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003228358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 842
ID ADH20071 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 843
ID ADJ54857 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 844
ID ADJ64628 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 845
ID ADM31524 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 846
ID ADM36571 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 847
ID ADM40376 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 848
ID ADN37994 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 12; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 849
ID AAV41257 standard; cDNA; 2082 BP.
DE Mouse neuronal PAS domain protein NPAS1 cDNA.
PN WO9831804-A1.
PD 23-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 10.8%; Score 61.8; DB 2; Length 2082;
Best Local Similarity 77.3%; Pred. No. 0.11;
RESULT 850
ID ACC69465 standard; cDNA; 2350 BP.
DE Human malignant neoplasm related protein encoding cDNA SEQ ID NO:1.
PN WO2003025135-A2.
PD 27-MAR-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.8%; Score 61.8; DB 8; Length 2350;
Best Local Similarity 77.3%; Pred. No. 0.11;
RESULT 851
ID ADK61480 standard; DNA; 246 BP.
DE Ovarian cancer-related DNA #635 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 10.8%; Score 61.6; DB 10; Length 246;
Best Local Similarity 76.0%; Pred. No. 0.11;
RESULT 852
ID ADK61470 standard; DNA; 320 BP.
DE Ovarian cancer-related DNA #625 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 10.8%; Score 61.6; DB 10; Length 320;

Best Local Similarity 73.1%; Pred. No. 0.11;
RESULT 853
ID ABV56614 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 56605.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 442;
Best Local Similarity 70.1%; Pred. No. 0.11;
RESULT 854
ID ABV48154 standard; cDNA; 458 BP.
DE Human prostate expression marker cDNA 48145.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 458;
Best Local Similarity 76.0%; Pred. No. 0.11;
RESULT 855
ID AAS41678 standard; cDNA; 524 BP.
DE cDNA encoding novel human enzyme polypeptide #894.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 61.6; DB 4; Length 524;
Best Local Similarity 79.3%; Pred. No. 0.11;
RESULT 856
ID ABV54778 standard; cDNA; 541 BP.
DE Human prostate expression marker cDNA 54769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 541;
Best Local Similarity 88.2%; Pred. No. 0.11;
RESULT 857
ID AAS29155 standard; cDNA; 713 BP.
DE cDNA encoding for human DNA-binding protein #126.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 61.6; DB 5; Length 713;
Best Local Similarity 79.3%; Pred. No. 0.12;
RESULT 858
ID ABS68295 standard; cDNA; 713 BP.
DE cDNA encoding human DNA-binding protein #126.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.8%; Score 61.6; DB 6; Length 713;
Best Local Similarity 79.3%; Pred. No. 0.12;
RESULT 859
ID ADC25289 standard; cDNA; 713 BP.
DE Human cDNA from extracellular matrix gene 126.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 61.6; DB 10; Length 713;
Best Local Similarity 79.3%; Pred. No. 0.12;
RESULT 860
ID AAS41417 standard; cDNA; 785 BP.
DE cDNA encoding novel human enzyme polypeptide #633.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 61.6; DB 4; Length 785;
Best Local Similarity 79.3%; Pred. No. 0.12;
RESULT 861
ID ADQ23347 standard; DNA; 1084 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8167.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 10.8%; Score 61.6; DB 12; Length 1084;
Best Local Similarity 88.2%; Pred. No. 0.12;
RESULT 862
ID ADB58406 standard; DNA; 1591 BP.
DE Toxicity-related gene, SEQ ID 3432.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.8%; Score 61.6; DB 10; Length 1591;
Best Local Similarity 83.3%; Pred. No. 0.12;
RESULT 863
ID ADB52986 standard; DNA; 1591 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3528.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.8%; Score 61.6; DB 10; Length 1591;
Best Local Similarity 83.3%; Pred. No. 0.12;
RESULT 864
ID ABR42053 standard; DNA; 1591 BP.
DE Toxicity modelling related rat gene SEQ ID NO 1755.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.8%; Score 61.6; DB 10; Length 1591;
Best Local Similarity 83.3%; Pred. No. 0.12;
RESULT 865
ID ACN39160 standard; cDNA; 2126 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325414, SEQ ID NO:3133.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.6; DB 13; Length 2126;
Best Local Similarity 65.0%; Pred. No. 0.12;
RESULT 866
ID ADP23018 standard; cDNA; 2126 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:112.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 61.6; DB 13; Length 2126;
Best Local Similarity 65.0%; Pred. No. 0.12;
RESULT 867
ID ABV23975 standard; cDNA; 2843 BP.
DE Human prostate expression marker cDNA 23966.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 2843;
Best Local Similarity 88.2%; Pred. No. 0.13;
RESULT 868
ID ABV24137 standard; cDNA; 2843 BP.
DE Human prostate expression marker cDNA 24128.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 2843;
Best Local Similarity 88.2%; Pred. No. 0.13;
RESULT 869
ID ABV20348 standard; cDNA; 2843 BP.
DE Human prostate expression marker cDNA 20339.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 2843;
Best Local Similarity 88.2%; Pred. No. 0.13;
RESULT 870
ID ABV20569 standard; cDNA; 2843 BP.
DE Human prostate expression marker cDNA 20560.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 61.6; DB 5; Length 2843;

Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 871
 ID ABV29860 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 29851.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 872
 ID ABV29747 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 29738.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 873
 ID ABV23968 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 23959.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 874
 ID ABV26408 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 26399.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 875
 ID ABV28716 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 28707.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 876
 ID ABV22885 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 22876.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 877
 ID ABV26181 standard; cDNA; 2843 BP.
 DE Human prostate expression marker cDNA 26172.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.6; DB 5; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 878
 ID ACN92620 standard; DNA; 2843 BP.
 DE Breast cancer related marker, seq id 13770.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.8%; Score 61.6; DB 11; Length 2843;
 Best Local Similarity 88.2%; Pred. No. 0.13;
 RESULT 879
 ID ABL92106 standard; cDNA; 4168 BP.
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 235.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 10.8%; Score 61.6; DB 6; Length 4168;
 Best Local Similarity 83.3%; Pred. No. 0.13;

RESULT 880
 ID ABX72031 standard; DNA; 4168 BP.
 DE DNA encoding human tumour endothelial marker TEM 21.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 10.8%; Score 61.6; DB 10; Length 4168;
 Best Local Similarity 83.3%; Pred. No. 0.13;
 RESULT 881
 ID ABV56502 standard; cDNA; 239 BP.
 DE Human prostate expression marker cDNA 56493.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.8%; Score 61.4; DB 5; Length 239;
 Best Local Similarity 91.5%; Pred. No. 0.12;
 RESULT 882
 ID ABL66854 standard; DNA; 257 BP.
 DE Lung cancer related gene sequence SEQ ID NO:5191.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AYAL-) AYALON PHARM.
 Query Match 10.8%; Score 61.4; DB 6; Length 257;
 Best Local Similarity 98.4%; Pred. No. 0.12;
 RESULT 883
 ID ABN96764 standard; DNA; 257 BP.
 DE Gene #3262 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.8%; Score 61.4; DB 6; Length 257;
 Best Local Similarity 98.4%; Pred. No. 0.12;
 RESULT 884
 ID ACN47867 standard; cDNA; 311 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-B4, SEQ:2648.
 PN US200412340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FING/) FINCHER K L.
 PA (ZIRG/) ZIEGLER T E.
 Query Match 10.8%; Score 61.4; DB 13; Length 311;
 Best Local Similarity 81.6%; Pred. No. 0.12;
 RESULT 885
 ID AAI84413 standard; cDNA; 332 BP.
 DE Human polynucleotide SEQ ID NO 4473.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 10.8%; Score 61.4; DB 4; Length 332;
 Best Local Similarity 73.2%; Pred. No. 0.12;
 RESULT 886
 ID AAI84912 standard; cDNA; 364 BP.
 DE Human polynucleotide SEQ ID NO 4972.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 10.8%; Score 61.4; DB 4; Length 364;
 Best Local Similarity 69.7%; Pred. No. 0.12;
 RESULT 887
 ID ABX44260 standard; cDNA; 377 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #9425.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 10.8%; Score 61.4; DB 8; Length 377;
 Best Local Similarity 77.9%; Pred. No. 0.12;
 RESULT 888
 ID ABV56784 standard; cDNA; 505 BP.
 DE Human prostate expression marker cDNA 56775.

PN WO200160860-A2.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PD 23-AUG-2001.
 Query Match 10.8%; Score 61.4; DB 5; Length 505;
 Best Local Similarity 91.5%; Pred. No. 0.12;
 RESULT 889
 ID AAI95102 standard; cDNA; 794 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1177.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM-) HISAMITSU PHARM CO LTD.
 Query Match 10.8%; Score 61.4; DB 4; Length 794;
 Best Local Similarity 66.4%; Pred. No. 0.13;
 RESULT 890
 ID ABA93750 standard; cDNA; 1316 BP.
 DE Human cell structure and motility cDNA clone test_16b5.
 PN WO200198454-A2.
 PD 27-DEC-2001.
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 Query Match 10.8%; Score 61.4; DB 6; Length 1316;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 891
 ID AAX16675 standard; DNA; 1554 BP.
 DE Xenopus WA545 protein encoding DNA.
 PN WO9902678-A1.
 PD 21-JAN-1999.
 PA (GEMV-) GENETICS INST INC.
 PA (WHEB-) WHITEHEAD INST BIOMEDICAL RES.
 Query Match 10.8%; Score 61.4; DB 2; Length 1554;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 892
 ID ABK35953 standard; cDNA; 1554 BP.
 DE cDNA sequence #344 encoding novel human secreted protein.
 PN WO200177289-A2.
 PD 18-OCT-2001.
 PA (GEMV-) GENETICS INST INC.
 Query Match 10.8%; Score 61.4; DB 6; Length 1554;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 893
 ID ADJ74992 standard; DNA; 1554 BP.
 DE Marker gene SEQ ID NO:244.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 10.8%; Score 61.4; DB 12; Length 1554;
 Best Local Similarity 65.9%; Pred. No. 0.13;
 RESULT 894
 ID AAX60810 standard; DNA; 1656 BP.
 DE Human secreted protein encoding DNA (clone yb8-1).
 PN WO9926961-A1.
 PD 03-JUN-1999.
 PA (GEMV-) GENETICS INST INC.
 Query Match 10.8%; Score 61.4; DB 2; Length 1656;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 895
 ID AAS59216 standard; cDNA; 1656 BP.
 DE Human cDNA encoding a secreted protein yb8_1.
 PN WO200175068-A2.
 PD 11-OCT-2001.
 PA (GEMV-) GENETICS INST INC.
 Query Match 10.8%; Score 61.4; DB 4; Length 1656;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 896
 ID ABA90885 standard; cDNA; 1656 BP.
 DE Human polynucleotide SEQ ID NO 19.
 PN US2001039335-A1.
 PD 08-NOV-2001.
 PA (JACO-) JACOBS K.
 PA (MCCO-) MCCOY J M.
 PA (LAVA-) LAVALLE E R.
 PA (COLL-) COLLINS-RACIE L A.
 PA (EVAN-) EVANS C.

PA (MERB-) MERBERG D.
 PA (TREB-) TREACY M.
 PA (AGOS-) AGOSTINO M J.
 PA (STRI-) STEININGER R J.
 PA (SPAU-) SPAULDING V.
 PA (WONG-) WONG G G.
 PA (CLAR-) CLARK H.
 PA (FECH-) FECHTEL K.
 Query Match 10.8%; Score 61.4; DB 6; Length 1656;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 897
 ID AAC98993 standard; cDNA; 1756 BP.
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:221.
 PN WO200055320-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.8%; Score 61.4; DB 3; Length 1756;
 Best Local Similarity 86.7%; Pred. No. 0.13;
 RESULT 898
 ID AAX20412 standard; DNA; 1761 BP.
 DE Human secreted protein gene 1.
 PN WO9906423-A1.
 PD 11-FEB-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.8%; Score 61.4; DB 2; Length 1761;
 Best Local Similarity 86.7%; Pred. No. 0.13;
 RESULT 899
 ID ADD90196 standard; cDNA; 1761 BP.
 DE Novel human secreted protein cDNA seq id 11.
 PN US2003199683-A1.
 PD 23-OCT-2003.
 PA (RUBE-) RUBEN S M.
 PA (FENG-) FENG P.
 PA (LAFU-) LAFLEUR D W.
 PA (MOOR-) MOORE P A.
 PA (SHIY-) SHI Y.
 PA (KYAM-) KYAM H.
 PA (LIYY-) LI Y.
 PA (ZENG-) ZENG Z.
 PA (CART-) CARTER K C.
 PA (ENDR-) ENDRESS G A.
 PA (WEIY-) WEI Y.
 PA (FANP-) FAN P.
 PA (ROSE-) ROSEN C A.
 Query Match 10.8%; Score 61.4; DB 10; Length 1761;
 Best Local Similarity 86.7%; Pred. No. 0.13;
 RESULT 900
 ID ADG90015 standard; cDNA; 1761 BP.
 DE Human cDNA from secreted protein gene 1.
 PN US2003165541-A1.
 PD 04-SEP-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.8%; Score 61.4; DB 10; Length 1761;
 Best Local Similarity 86.7%; Pred. No. 0.13;
 RESULT 901
 ID AAZ33323 standard; cDNA; 2364 BP.
 DE Human secreted protein clone pm749_8 nucleotide sequence SEQ ID NO:15.
 PN WO9957132-A1.
 PD 11-NOV-1999.
 PA (GEMV-) GENETICS INST INC.
 Query Match 10.8%; Score 61.4; DB 3; Length 2364;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 902
 ID ABL34984 standard; cDNA; 2538 BP.
 DE Rat cDNA isolated from skin cells SEQ ID NO: 511.
 PN WO200190357-A1.
 PD 29-NOV-2001.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 10.8%; Score 61.4; DB 6; Length 2538;
 Best Local Similarity 91.5%; Pred. No. 0.13;
 RESULT 903
 ID AAF28356 standard; cDNA; 2850 BP.
 DE Human BSR Gene X cDNA.

PN WO200100825-A2.
PD 04-JAN-2001.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 10.8%; Score 61.4; DB 4; Length 2850;
RESULT 904
ID AAS14756 standard; cDNA; 2968 BP.
DE Human protease cDNA.
PN US6294368-B1.
PD 25-SEP-2001.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 10.8%; Score 61.4; DB 5; Length 2968;
RESULT 905
ID ABL41523 standard; cDNA; 2968 BP.
DE Human metalloprotease encoding sequence.
PN US6344352-B1.
PD 05-FEB-2002.
PA (PEKE) PE CORP.
Query Match
Best Local Similarity 10.8%; Score 61.4; DB 6; Length 2968;
RESULT 906
ID ADG47800 standard; cDNA; 2968 BP.
DE Human protease cDNA.
PN US2002137183-A1.
PD 26-SEP-2002.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 10.8%; Score 61.4; DB 12; Length 2968;
RESULT 907
ID ABZ23375 standard; cDNA; 445 BP.
DE Reverse complement of oestrogen receptor alpha cofactor CF17 cDNA.
PN WO200270689-A2.
PD 12-SEP-2002.
PA (LION-) LION BIOSCIENCE AG.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 445;
RESULT 908
ID ABZ23374 standard; cDNA; 445 BP.
DE Nucleotide sequence of oestrogen receptor alpha cofactor CF17.
PN WO200270689-A2.
PD 12-SEP-2002.
PA (LION-) LION BIOSCIENCE AG.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 445;
RESULT 909
ID ACN87190 standard; DNA; 592 BP.
DE Breast cancer related marker, seq id 8340.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 11; Length 592;
RESULT 910
ID AAV58509 standard; cDNA; 789 BP.
DE 3' fragment of prostate tumour specific gene J1-21.
PN WO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 2; Length 789;
RESULT 911
ID AAV61275 standard; cDNA; 789 BP.
DE 3' cDNA sequence of prostate tumour clone J1-21.
PN WO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 2; Length 789;
RESULT 912
ID AAA06272 standard; cDNA; 789 BP.
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:32.
PN WO200004149-A2.

PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 3; Length 789;
RESULT 913
ID ABS71177 standard; cDNA; 789 BP.
DE Human prostate tumour protein partial DNA sequence #32.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUJ/) XU J.
PA (DILL-) DILLON D C.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 3; Length 789;
RESULT 914
ID AAH93388 standard; cDNA; 789 BP.
DE Human prostate-specific 3' cDNA sequence J1-21.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;
RESULT 915
ID AAS63480 standard; cDNA; 789 BP.
DE Human prostate cDNA sequence #32.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;
RESULT 916
ID AAH02453 standard; cDNA; 789 BP.
DE Prostate tumour antigen determined 3' cDNA sequence for J1-21.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;
RESULT 917
ID AAH84702 standard; cDNA; 789 BP.
DE Human prostate-specific 3' cDNA sequence J1-21.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;
RESULT 918
ID ACA59289 standard; cDNA; 789 BP.
DE Prostate cancer therapy associated cDNA #32.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL-) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HART/) HARLOCKER S L.
PA (UTAN/) UTANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNETILL P D.
PA (HOUN/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOYT T M.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 5; Length 789;

Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 919
ID AAS10031 standard; cDNA; 789 BP.
DE Human prostate tumour cDNA J1-21.
PN US6262245-A1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.7%; Score 61.2; DB 5; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 920
ID ABL94852 standard; cDNA; 789 BP.
DE Human J1-21 3' cDNA sequence SEQ ID NO 32.
PN US200202248-A1.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKET/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match 10.7%; Score 61.2; DB 6; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 921
ID ABS58561 standard; cDNA; 789 BP.
DE Prostate tumour cDNA #32.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 10.7%; Score 61.2; DB 6; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 922
ID ACC95016 standard; cDNA; 789 BP.
DE Prostate tumour specific cDNA sequence SEQ ID 32.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.7%; Score 61.2; DB 8; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 923
ID ADB13482 standard; cDNA; 789 BP.
DE Human prostate specific cDNA J1-21.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.7%; Score 61.2; DB 10; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 924
ID ADG26898 standard; cDNA; 789 BP.
DE Human prostate-specific cDNA #32.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.7%; Score 61.2; DB 10; Length 789;
Best Local Similarity 81.2%; Pred. No. 0.14;
RESULT 925
ID AAA78426 standard; cDNA; 1028 BP.
DE Human secreted protein gene 46 SEQ ID NO:56.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61.2; DB 3; Length 1028;

Best Local Similarity 60.4%; Pred. No. 0.14;
RESULT 926
ID AAS29631 standard; cDNA; 1437 BP.
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 131.
PN WO200155364-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61.2; DB 5; Length 1437;
Best Local Similarity 66.9%; Pred. No. 0.14;
RESULT 927
ID AAS02065 standard; cDNA; 1477 BP.
DE Human MANGO 511 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 61.2; DB 4; Length 1477;
Best Local Similarity 73.6%; Pred. No. 0.14;
RESULT 928
ID AAS02102 standard; cDNA; 1477 BP.
DE Human MANGO 511, variant #1 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 61.2; DB 4; Length 1477;
Best Local Similarity 73.6%; Pred. No. 0.14;
RESULT 929
ID AAS02104 standard; cDNA; 1477 BP.
DE Human MANGO 511, variant #3 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 61.2; DB 4; Length 1477;
Best Local Similarity 73.6%; Pred. No. 0.14;
RESULT 930
ID AAS02105 standard; cDNA; 1477 BP.
DE Human MANGO 511, variant #4 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 61.2; DB 4; Length 1477;
Best Local Similarity 73.6%; Pred. No. 0.14;
RESULT 931
ID AAS02103 standard; cDNA; 1477 BP.
DE Human MANGO 511, variant #2 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 61.2; DB 4; Length 1477;
Best Local Similarity 73.6%; Pred. No. 0.14;
RESULT 932
ID ABQ54407 standard; cDNA; 1898 BP.
DE Human ovarian antigen HBST67 cDNA, SEQ ID NO:287.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61.2; DB 6; Length 1898;
Best Local Similarity 89.2%; Pred. No. 0.14;
RESULT 933
ID AAZ41321 standard; cDNA; 2042 BP.
DE Human normal ovarian tissue derived cDNA 100.
PN DE19816395-A1.
PD 07-OCT-1999.
PA (MERA-) METAGEN GBS GENOMFORSCHUNG MBH.
Query Match 10.7%; Score 61.2; DB 2; Length 2042;
Best Local Similarity 89.2%; Pred. No. 0.14;
RESULT 934
ID AAS31306 standard; cDNA; 2272 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID NO 120.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61.2; DB 4; Length 2272;
Best Local Similarity 71.1%; Pred. No. 0.15;

RESULT 935
ID ABO6630 standard; cDNA; 2272 BP.
DE Human polynucleotide SEQ ID NO 120.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARRASH S C.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 2272;
RESULT 936
ID ADCl0652 standard; cDNA; 2272 BP.
DE Human cDNA from extracellular matrix gene 110.
PN US2003058875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2272;
RESULT 937
ID ACN88739 standard; DNA; 2310 BP.
DE Breast cancer related marker, seq id 9889.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 11; Length 2310;
RESULT 938
ID AAD05588 standard; cDNA; 2762 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HTUML75, SEQ ID NO:20.
PN WO200134627-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 2762;
RESULT 939
ID ADA40188 standard; cDNA; 2762 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 8; Length 2762;
RESULT 940
ID ADC73727 standard; DNA; 2762 BP.
DE Human secreted protein-related DNA - SEQ ID 360.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2762;
RESULT 941
ID ADA56348 standard; DNA; 2762 BP.
DE Gene encoding human secreted protein #527.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2762;
RESULT 942
ID ADJ48200 standard; DNA; 3505 BP.
DE Maize oil-associated gene #18.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDER J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 10.7%; Score 61.2; DB 12; Length 3505;
RESULT 943
ID ABV59005 standard; cDNA; 196 BP.
DE Human prostate expression marker cDNA 58996.
PN

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 5; Length 196;
RESULT 944
ID ABZ08427 standard; cDNA; 290 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8418.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 6; Length 290;
RESULT 945
ID ABV60857 standard; cDNA; 352 BP.
DE Human prostate expression marker cDNA 60848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 5; Length 352;
RESULT 946
ID AA185189 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 3249.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 4; Length 417;
RESULT 947
ID AA188584 standard; cDNA; 427 BP.
DE Human polynucleotide SEQ ID NO 8644.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 4; Length 427;
RESULT 948
ID ADL43473 standard; DNA; 438 BP.
DE Human ovarian cancer DNA marker #17363.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 10.7%; Score 61; DB 5; Length 438;
RESULT 949
ID ACH28067 standard; cDNA; 488 BP.
DE Human adult ovary cDNA #6447.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 10.7%; Score 61; DB 9; Length 488;
RESULT 950
ID ACH22923 standard; cDNA; 489 BP.
DE Human adult ovary cDNA #1303.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 10.7%; Score 61; DB 9; Length 489;
RESULT 951
ID AAS29116 standard; cDNA; 583 BP.
DE cDNA encoding for human DNA-binding protein #87.
PN WO200155162-A1.
PN

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61; DB 5; Length 583;
Best Local Similarity 70.1%; Pred. No. 0.14;
RESULT 952
ID ABS68256 standard; cDNA; 583 BP.
DE cDNA encoding human DNA-binding protein #87.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.7%; Score 61; DB 6; Length 583;
Best Local Similarity 70.1%; Pred. No. 0.14;
RESULT 953
ID ADC25250 standard; cDNA; 583 BP.
DE Human cDNA from extracellular matrix gene 87.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61; DB 10; Length 583;
Best Local Similarity 70.1%; Pred. No. 0.14;
RESULT 954
ID AAV58363 standard; cDNA; 772 BP.
DE Coding sequence for secreted protein of clone EQ219_1.
PN WO9837094-A2.
PD 27-AUG-1998.
PA (GEM/) GENETICS INST INC.
Query Match 10.7%; Score 61; DB 2; Length 772;
Best Local Similarity 82.4%; Pred. No. 0.15;
RESULT 955
ID AAT70132 standard; cDNA to mRNA; 1023 BP.
DE Max-interacting protein coding sequence (clone 20).
PN US5624818-A.
PD 29-APR-1997.
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
Query Match 10.7%; Score 61; DB 2; Length 1023;
Best Local Similarity 64.5%; Pred. No. 0.15;
RESULT 956
ID AAF21764 standard; DNA; 1066 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 151.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61; DB 3; Length 1066;
Best Local Similarity 60.2%; Pred. No. 0.15;
RESULT 957
ID AAQ05879 standard; DNA; 1394 BP.
DE Placenta-specific protein-9 gene.
PN EP386733-A.
PD 12-SEP-1990.
PA (BEHW) BEHRINGER AG.
Query Match 10.7%; Score 61; DB 2; Length 1394;
Best Local Similarity 87.0%; Pred. No. 0.15;
RESULT 958
ID AAF97914 standard; cDNA; 1651 BP.
DE Human secreted protein cDNA, SEQ ID NO: 41.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61; DB 4; Length 1651;
Best Local Similarity 64.9%; Pred. No. 0.15;
RESULT 959
ID ADQ24380 standard; DNA; 1781 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7200.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.7%; Score 61; DB 12; Length 1781;
Best Local Similarity 78.5%; Pred. No. 0.15;
RESULT 960
ID AAC90463 standard; cDNA; 2517 BP.
DE Human uncoupling protein cDNA #12.

PN WO200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 61; DB 3; Length 2517;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 961
ID AAS75804 standard; cDNA; 2891 BP.
DE DNA encoding novel human diagnostic protein #11608.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 61; DB 5; Length 2891;
Best Local Similarity 78.5%; Pred. No. 0.16;
RESULT 962
ID AAZ65058 standard; cDNA; 3333 BP.
DE Membrane-bound protein PRO1106 encoding cDNA.
PN WO963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 3; Length 3333;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 963
ID AAF92086 standard; cDNA; 3334 BP.
DE Human PRO1106 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 4; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 964
ID AAF44204 standard; cDNA; 3334 BP.
DE Human PRO1106 (UNQ549) nucleotide sequence SEQ ID NO:288.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 5; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 965
ID ABS74406 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 6; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 966
ID ACA64351 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 967
ID ACA91192 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 968
ID ACD81569 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 969
ID ACA60391 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003018183-A1.

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PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 970
ID AC658838 standard; cDNA; 3334 BP.
DE cDNA encoding human secreted polypeptide PRO1106.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 971
ID AC6464014 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO polypeptide #29.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 972
ID AC691278 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO polypeptide #29.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 973
ID ABX80810 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane protein cDNA, #118.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 974
ID AC644319 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO1106 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 975
ID AC645177 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane polypeptide PRO1106 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 976
ID AC693725 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 977
ID AC67299 standard; cDNA; 3334 BP.
DE cDNA encoding human secreted polypeptide PRO1106.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 978
ID AC666272 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 979
ID AC679490 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane protein cDNA, #118.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 980
ID AC693511 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 981
ID ABX81193 standard; DNA; 3334 BP.
DE Novel human secreted or transmembrane protein PRO1291 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 982
ID ACD02326 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 983
ID AC689317 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 984
ID AC68954 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 985
ID AC693009 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 986
ID AC698476 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 987
ID ABX17093 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 8; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 988
ID AC67948 standard; cDNA; 3334 BP.
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DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 989
ID ACA63401 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO polypeptide #29.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 990
ID ACA88397 standard; cDNA; 3334 BP.
DE Human secreted and transmembrane polypeptide PRO1106 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 991
ID ACD81904 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO1106 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 992
ID ADB17114 standard; cDNA; 3334 BP.
DE Human cDNA clone (SeqID 57) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 993
ID ADA37799 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 994
ID ADA21485 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1106.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 995
ID ACH03604 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane polypeptide PRO 11106 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 996
ID ADA10272 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1106.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 997
ID ADA19919 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 998
ID ADB17302 standard; cDNA; 3334 BP.
DE Human cDNA clone (SeqID 57) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 999
ID ADA17816 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO1106 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1000
ID ADA27924 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1001
ID ADA20091 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1002
ID ACD82118 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane polypeptide PRO 11106 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1003
ID ADA94504 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1004
ID ADA38729 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1005
ID ADA92850 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1006
ID ADA00388 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane polypeptide PRO 1106 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1007
ID ACH65465 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003044806-A1.

PD 06-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1008
ID ADA22411 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1106.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1009
ID ACD39455 standard; cDNA; 3334 BP.
DE Human cDNA encoding PRO1291.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1010
ID ADA06577 standard; cDNA; 3334 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #88.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1011
ID ADA39270 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1012
ID ADH85630 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1013
ID ADB96296 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1014
ID ADB68309 standard; cDNA; 3334 BP.
DE Human PRO1106 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
Query Match 10.7%; Score 61; DB 9; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1015
ID ADB68116 standard; cDNA; 3334 BP.
DE Human PRO1106 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1016
ID ADB90933 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1017
ID ADC57768 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.

PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1018
ID ADC55132 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1019
ID ADC11999 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1020
ID ADC07013 standard; cDNA; 3334 BP.
DE Human PRO1106 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1021
ID ADC56423 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1022
ID ADC17192 standard; cDNA; 3334 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 57).
PN US2003065143-A1.
PD 03-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1023
ID ADC07476 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1024
ID ADC11466 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1025
ID ADC14890 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1026
ID ADC52385 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1027
ID ADC14588 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1028
ID ADD08120 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1029
ID ADC81945 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003063461-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1030
ID ADD07587 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1031
ID ADC82478 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1032
ID ADD08658 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1033
ID ADD06907 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1034
ID ADC83154 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1035
ID ADD55261 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1036
ID ADD30661 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1037
ID ADD56219 standard; cDNA; 3334 BP.

DE Human PRO polynucleotide #88.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1038
ID ADD54657 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1039
ID ADE26811 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1040
ID ADE26278 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1041
ID ADF67215 standard; cDNA; 3334 BP.
DE Human PRO1106 nucleotide sequence SEQ ID NO:288.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1042
ID ADG01062 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1043
ID ADG08615 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1044
ID ADF95236 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1045
ID ADH24089 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1046
ID ADH34115 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1047
ID ADH29948 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1048
ID ADH23919 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1049
ID ADG85323 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1050
ID ADH24599 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1051
ID ADH37455 standard; cDNA; 3334 BP.
DE Human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1052
ID ADH02044 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1053
ID ADH37625 standard; cDNA; 3334 BP.
DE Human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1054
ID ADG85663 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1055
ID ADH24259 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;

Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1056
ID ADH38553 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1057
ID ADG83674 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1058
ID ADH29482 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1059
ID ADH27598 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1060
ID ADH37795 standard; cDNA; 3334 BP.
DE Human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1061
ID ADH37972 standard; cDNA; 3334 BP.
DE Human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1062
ID ADH57392 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1063
ID ADH53534 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1064
ID ADH53704 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;

RESULT 1065
ID ADH52040 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1066
ID ADH49895 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1067
ID ADI25405 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1068
ID ADH90198 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1069
ID ADI25575 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1070
ID ADH97749 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1071
ID ADI35469 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1072
ID ADI03597 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1073
ID ADI11954 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1074
ID ADH90028 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1075
ID ADH99961 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1076
ID ADH98429 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1077
ID ADI11104 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1078
ID ADI11614 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1079
ID ADH98259 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1080
ID ADH98599 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1081
ID ADH98089 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1082
ID ABX77894 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #88.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1083
ID ABX80306 standard; cDNA; 3334 BP.
DE Novel human secreted or transmembrane protein PRO1291 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.

RESULT 1102
ID AD104621 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1103
ID ADH79493 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1104
ID AD119450 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1105
ID AD105251 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1106
ID ADH79663 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1107
ID AD101489 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1108
ID AD101659 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1109
ID AD101829 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1110
ID ADH79833 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1111

ID AD104651 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1112
ID AD102787 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1113
ID ADH78106 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1114
ID AD125745 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1115
ID AD125915 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1116
ID ADK65427 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1117
ID ADH98769 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1118
ID ADH80010 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1119
ID ADL93741 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 11; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1120
ID ADC52195 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003130483-A1.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1121
ID ADF35414 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO1106 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1122
ID ADG11664 standard; cDNA; 3334 BP.
DE cDNA encoding human PRO1106 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1123
ID ADH06627 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1124
ID ADH06457 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1125
ID ADG68878 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1126
ID ADH27768 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1127
ID ADH25109 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1128
ID ADH33741 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1129
ID ADH02384 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180839-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1130
ID ADH07991 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1131
ID ADG69388 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1132
ID ADH39209 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1133
ID ADG83949 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1134
ID ADH19534 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1135
ID ADG85493 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US200316848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1136
ID ADH06287 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1137
ID ADH30117 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1138
ID ADH24429 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1139
ID ADG69558 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1140
ID ADH07821 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1141
ID ADG85833 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1142
ID ADH3379 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1143
ID ADH33571 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1144
ID ADH33911 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1145
ID ADH01121 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1146
ID ADG69728 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1147
ID ADH21027 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US200324358-A1.
PD 04-DEC-2003.
Query Match 10.7%; Score 61; DB 12; Length 3334;

Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1148
ID ADH02214 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1149
ID ADG69218 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1150
ID ADG86003 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1151
ID ADH24939 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1152
ID ADH35556 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1153
ID ADH20067 standard; cDNA; 3334 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1106.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1154
ID ADH02554 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1155
ID ADG69048 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1156
ID ADH07651 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;

RESULT 1157
ID ADG86173 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1158
ID ADH24769 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1159
ID ADH25817 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1160
ID ADH38383 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1161
ID ADH52209 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1162
ID ADH52209 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1163
ID ADH49576 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1164
ID ADH90538 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1165
ID ADI11274 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1166
ID ADH79082 standard; cDNA; 3334 BP.

ID ADH98939 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1167
ID ADI02169 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1168
ID ADH90708 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1169
ID ADJ98583 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1170
ID ADJ98753 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1171
ID ADH78912 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1172
ID ADJ99146 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1173
ID ADJ99316 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1174
ID ADJ98934 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1175
ID ADH79082 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1176
ID ADK00942 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1177
ID ADK14463 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1178
ID ADM80912 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 61; DB 12; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1179
ID AAI58310 standard; cDNA; 4419 BP.
DE Human polynucleotide SEQ ID NO 513.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 61; DB 4; Length 4419;
Best Local Similarity 58.6%; Pred. No. 0.16;
RESULT 1180
ID ADQ98517 standard; cDNA; 4419 BP.
DE DNA encoding human GPCR-like protein seqid 187.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 61; DB 5; Length 4419;
Best Local Similarity 58.6%; Pred. No. 0.16;
RESULT 1181
ID ADB48277 standard; cDNA; 4419 BP.
DE Novel human cDNA SEQ ID NO 187.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 10.7%; Score 61; DB 9; Length 4419;
Best Local Similarity 58.6%; Pred. No. 0.16;
RESULT 1182
ID ABV58256 standard; cDNA; 304 BP.
DE Human prostate expression marker cDNA 58247.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.7%; Score 60.8; DB 5; Length 304;
Best Local Similarity 89.0%; Pred. No. 0.15;
RESULT 1183
ID ACN88196 standard; DNA; 375 BP.
DE Breast cancer related marker, seq id 9346.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 60.8; DB 11; Length 375;

Best Local Similarity 71.3%; Pred. No. 0.15;
RESULT 1184
ID ADF50926 standard; cDNA; 400 BP.
DE Human cysteine rich intestinal protein 1 cDNA (seqid 25).
PN WO2003060164-A1.
PD 24-JUL-2003.
PA (ARCT-) ARCTURUS ENG INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 10.7%; Score 60.8; DB 10; Length 400;
Best Local Similarity 80.7%; Pred. No. 0.15;
RESULT 1185
ID AAI86835 standard; cDNA; 435 BP.
DE Human polynucleotide SEQ ID NO 6895.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 60.8; DB 4; Length 435;
Best Local Similarity 90.3%; Pred. No. 0.15;
RESULT 1186
ID ACN49982 standard; cDNA; 441 BP.
DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F1, SEQ:4763.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.7%; Score 60.8; DB 13; Length 441;
Best Local Similarity 69.2%; Pred. No. 0.15;
RESULT 1187
ID ABV58572 standard; cDNA; 455 BP.
DE Human prostate expression marker cDNA 58563.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.7%; Score 60.8; DB 5; Length 455;
Best Local Similarity 87.8%; Pred. No. 0.15;
RESULT 1188
ID ACN51998 standard; cDNA; 464 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E3, SEQ:6779.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.7%; Score 60.8; DB 13; Length 464;
Best Local Similarity 80.7%; Pred. No. 0.15;
RESULT 1189
ID ACH39052 standard; cDNA; 465 BP.
DE Human foetal brain cDNA #419.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.7%; Score 60.8; DB 9; Length 465;
Best Local Similarity 70.2%; Pred. No. 0.15;
RESULT 1190
ID ACN56061 standard; cDNA; 474 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-F7, SEQ:10842.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.7%; Score 60.8; DB 13; Length 474;
Best Local Similarity 80.7%; Pred. No. 0.15;
RESULT 1191
ID ACH44386 standard; cDNA; 493 BP.

DE Human foetal brain cDNA #5111.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON W C.
 PA (JONE/) JONES L W.
 Query Match 10.7%; Score 60.8; DB 9; Length 493;
 Best Local Similarity 90.3%; Pred. No. 0.15;
 RESULT 1192
 ID ABV5433 standard; cDNA; 499 BP.
 DE Human prostate expression marker cDNA 54324.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.7%; Score 60.8; DB 5; Length 499;
 Best Local Similarity 89.0%; Pred. No. 0.15;
 RESULT 1193
 ID ACN61287 standard; cDNA; 512 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-035-Q1-N6-E12, SEQ:16066.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIRG/) ZIEGLER T E.
 Query Match 10.7%; Score 60.8; DB 13; Length 512;
 Best Local Similarity 80.7%; Pred. No. 0.16;
 RESULT 1194
 ID AAS60634 standard; cDNA; 520 BP.
 DE Human cancer agent-resistance marker #389.
 PN WO200179556-A2.
 PD 25-OCT-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.7%; Score 60.8; DB 4; Length 520;
 Best Local Similarity 80.7%; Pred. No. 0.16;
 RESULT 1195
 ID ABV58049 standard; cDNA; 564 BP.
 DE Human prostate expression marker cDNA 58040.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.7%; Score 60.8; DB 5; Length 564;
 Best Local Similarity 89.0%; Pred. No. 0.16;
 RESULT 1196
 ID ACN87651 standard; DNA; 635 BP.
 DE Breast cancer related marker, seq id 8801.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.7%; Score 60.8; DB 11; Length 635;
 Best Local Similarity 78.0%; Pred. No. 0.16;
 RESULT 1197
 ID ADN37279 standard; cDNA; 663 BP.
 DE Wheat chaumatin-like protein encoding cDNA SEQ ID NO:23.
 PN WO2004035790-A1.
 PD 29-APR-2004.
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.
 PA (GRAI-) GRAINS RES & DEV CORP.
 Query Match 10.7%; Score 60.8; DB 12; Length 663;
 Best Local Similarity 85.0%; Pred. No. 0.16;
 RESULT 1199
 ID ABQ54901 standard; cDNA; 783 BP.

DE Human ovarian antigen HLYAR61 cDNA, SEQ ID NO:781.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.7%; Score 60.8; DB 6; Length 783;
 Best Local Similarity 85.0%; Pred. No. 0.16;
 RESULT 1200
 ID ACC00704 standard; cDNA; 1249 BP.
 DE Zea mays oil trait related cDNA sequence SEQ ID NO:157.
 PN WO2003002751-A2.
 PD 09-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 10.7%; Score 60.8; DB 8; Length 1249;
 Best Local Similarity 65.4%; Pred. No. 0.16;
 RESULT 1201
 ID ADQ23409 standard; DNA; 1302 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6229.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 10.7%; Score 60.8; DB 12; Length 1302;
 Best Local Similarity 65.4%; Pred. No. 0.16;
 RESULT 1202
 ID AAD17173 standard; cDNA; 1779 BP.
 DE Human ion channel-31d6 (ion31d6) cDNA.
 PN WO200168849-A2.
 PD 20-SEP-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 10.7%; Score 60.8; DB 4; Length 1779;
 Best Local Similarity 71.4%; Pred. No. 0.17;
 RESULT 1203
 ID ACD01559 standard; cDNA; 1779 BP.
 DE cDNA clone Ion31c4 encoding human ion channel.
 PN WO2003023014-A2.
 PD 20-MAR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 10.7%; Score 60.8; DB 8; Length 1779;
 Best Local Similarity 71.4%; Pred. No. 0.17;
 RESULT 1204
 ID ADE29300 standard; cDNA; 1779 BP.
 DE Novel human ion channel ion-31d6 cDNA.
 PN US2003190714-A1.
 PD 09-OCT-2003.
 PA (ROBE/) ROBERTS S L.
 PA (BENU/) BENJAMIN C W.
 PA (KARN/) KARNOVSKY A M.
 PA (RUBI/) RUBLE C L.
 PA (LINS/) LINSKE-O'CONNELL L I.
 PA (WANG/) WANG.
 PA (LIUD/) LIU D.
 Query Match 10.7%; Score 60.8; DB 10; Length 1779;
 Best Local Similarity 71.4%; Pred. No. 0.17;
 RESULT 1205
 ID ABS57347 standard; cDNA; 1851 BP.
 DE cDNA encoding human cancer cell growth suppressing protein pP6068.
 PN CN1351080-A.
 PD 29-MAY-2002.
 PA (SHAN-) SHANGHAI INST ONCOLOGY.
 Query Match 10.7%; Score 60.8; DB 6; Length 1851;
 Best Local Similarity 77.1%; Pred. No. 0.17;
 RESULT 1206
 ID AAC81052 standard; cDNA; 1859 BP.
 DE Human secreted protein cDNA sequence #25.
 PN WO200063330-A2.
 PD 26-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.7%; Score 60.8; DB 3; Length 1859;
 Best Local Similarity 85.0%; Pred. No. 0.17;
 RESULT 1207
 ID ACD01569 standard; DNA; 1865 BP.
 DE DNA clone SHT-3C encoding human ion channel.
 PN WO2003023014-A2.

PD 20-MAR-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 10.7%; Score 60.8; DB 8; Length 1865;
Best Local Similarity 71.4%; Pred. No. 0.17;
RESULT 1208
ID ABK14606 standard; DNA; 2131 BP.
DE DNA encoding novel human ion channel, 5HT3C.
PN WO200202639-A2.
PD 10-JUN-2002.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 10.7%; Score 60.8; DB 6; Length 2131;
Best Local Similarity 71.4%; Pred. No. 0.17;
RESULT 1209
ID ADE54669 standard; DNA; 2287 BP.
DE Human gene NM_003026, SEQ ID NO 474.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.7%; Score 60.8; DB 10; Length 2287;
Best Local Similarity 90.3%; Pred. No. 0.17;
RESULT 1210
ID AAC76596 standard; cDNA; 2429 BP.
DE Human ORFX ORF2151 polynucleotide sequence SEQ ID NO:4301.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 60.8; DB 3; Length 2429;
Best Local Similarity 90.3%; Pred. No. 0.17;
RESULT 1211
ID AAD05229 standard; cDNA; 3143 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HHEP23, SEQ ID NO:20.
PN WO200134629-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 60.8; DB 4; Length 3143;
Best Local Similarity 63.9%; Pred. No. 0.17;
RESULT 1212
ID AA161619 standard; cDNA; 3508 BP.
DE Human secreted protein clone 10311_8 nucleotide sequence SEQ ID NO:3.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 10.7%; Score 60.8; DB 3; Length 3508;
Best Local Similarity 85.0%; Pred. No. 0.17;
RESULT 1213
ID ACN47721 standard; cDNA; 180 BP.
DE Cotton primed seed EST Clone ID: LIB3825-014-Q1-K6-B9, SEQ:2502.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.6%; Score 60.6; DB 13; Length 180;
Best Local Similarity 79.1%; Pred. No. 0.16;
RESULT 1214
ID ABV58603 standard; cDNA; 267 BP.
DE Human prostate expression marker cDNA 58594.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.6%; Score 60.6; DB 5; Length 267;
Best Local Similarity 69.8%; Pred. No. 0.16;
RESULT 1215
ID ACN54560 standard; cDNA; 432 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-D3, SEQ:9341.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

Query Match 10.6%; Score 60.6; DB 13; Length 432;
Best Local Similarity 75.0%; Pred. No. 0.17;
RESULT 1216
ID ADC38691 standard; cDNA; 438 BP.
DE Human cDNA encoding a secreted protein #25.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 10.6%; Score 60.6; DB 10; Length 438;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1217
ID ACH22246 standard; cDNA; 460 BP.
DE Human adult ovary cDNA #626.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.6%; Score 60.6; DB 9; Length 460;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1218
ID AA185012 standard; cDNA; 497 BP.
DE Human polynucleotide SEQ ID NO 5072.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 60.6; DB 4; Length 497;
Best Local Similarity 78.4%; Pred. No. 0.17;
RESULT 1219
ID ACN54072 standard; cDNA; 640 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.
PN US200413340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 10.6%; Score 60.6; DB 13; Length 640;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1220
ID AAN40162 standard; cDNA; 766 BP.
DE Sequence of preproparathyroid cDNA.
PN WO8401173-A.
PD 29-MAR-1984.
PA (IMMU-) IMMUNO NUCLEAR CORP.
Query Match 10.6%; Score 60.6; DB 1; Length 766;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1221
ID AAC74426 standard; cDNA; 860 BP.
DE Human secreted protein gene 31 SEQ ID NO:41.
PN WO200058496-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 60.6; DB 3; Length 860;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1222
ID AAT72173 standard; cDNA to mRNA; 882 BP.
DE Alzheimer's disease DNA sequence from plaamid pGCS1180.
PN WO9721807-A1.
PD 19-JUN-1997.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 10.6%; Score 60.6; DB 2; Length 882;
Best Local Similarity 88.0%; Pred. No. 0.17;
RESULT 1223
ID AAC89723 standard; cDNA; 1091 BP.
DE Maize Zmgent1-1 glucanase cDNA.
PN WO200073470-A2.
PD 07-DEC-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 10.6%; Score 60.6; DB 4; Length 1091;
Best Local Similarity 88.0%; Pred. No. 0.18;

RESULT 1224	PN US2003036162-A1.
ID ABX95035 standard; cDNA; 1091 BP.	PD 20-FEB-2003.
DE cDNA encoding maize coleoptile endo-1,3;1,4-beta-glucanase.	PA (GETH) GENENTECH INC.
PN US6501008-B1.	Query Match
PD 31-DEC-2002.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PA (REGC) UNIV CALIFORNIA.	79.1%; Pred. No. 0.18;
Query Match	RESULT 1234
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1091;	ID ACA6652 standard; cDNA; 1234 BP.
RESULT 1225	DE cDNA encoding human PRO protein #119.
ID AAA39072 standard; cDNA; 1157 BP.	PD US2003036137-A1.
DE Human secreted protein gene 21 SEQ ID NO:31.	PD 20-FEB-2003.
PN WO200017222-A1.	PA (GETH) GENENTECH INC.
PD 30-MAR-2000.	Query Match
PA (HDMA-) HUMAN GENOME SCI INC.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
Query Match	RESULT 1235
Best Local Similarity 10.6%; Score 60.6; DB 3; Length 1157;	ID ACA91195 standard; cDNA; 1234 BP.
RESULT 1226	DE Novel human secreted and transmembrane protein PRO3566 cDNA.
ID ACN40941 standard; cDNA; 1194 BP.	PN US2003016173-A1.
DE Tumour-associated antigenic target (TAT) cDNA DNA36971, SEQ ID NO:6056.	PD 23-JAN-2003.
PN WO2004030615-A2.	PA (GETH) GENENTECH INC.
PD 15-APR-2004.	Query Match
PA (GETH) GENENTECH INC.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
Query Match	RESULT 1236
Best Local Similarity 10.6%; Score 60.6; DB 13; Length 1194;	ID ACD81572 standard; cDNA; 1234 BP.
RESULT 1227	DE Human cDNA encoding secreted/transmembrane protein PRO3566.
ID ACC74280 standard; cDNA; 1233 BP.	PN US2003009013-A1.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.	PD 09-JAN-2003.
PN US2003027275-A1.	PA (GETH) GENENTECH INC.
PD 06-FEB-2003.	Query Match
Query Match	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1233;	RESULT 1237
RESULT 1228	ID ACP20227 standard; cDNA; 1234 BP.
ID AAS46043 standard; cDNA; 1234 BP.	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237
DE Human DNA encoding PRO polypeptide sequence #119.	PN US2003040063-A1.
PN WO2001168848-A2.	PD 27-FEB-2003.
PD 20-SEP-2001.	Query Match
PA (GETH) GENENTECH INC.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
Query Match	RESULT 1238
Best Local Similarity 10.6%; Score 60.6; DB 4; Length 1234;	ID ACEF19613 standard; cDNA; 1234 BP.
RESULT 1229	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237
ID AAP92089 standard; cDNA; 1234 BP.	PN US2003040064-A1.
DE Human PRO3566 cDNA.	PD 27-FEB-2003.
PN WO200116318-A2.	Query Match
PD 08-MAR-2001.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PA (GETH) GENENTECH INC.	RESULT 1239
Query Match	ID ACD21901 standard; cDNA; 1234 BP.
Best Local Similarity 10.6%; Score 60.6; DB 4; Length 1234;	DE Human secreted/transmembrane protein (PRO) cDNA #119.
RESULT 1230	PN US2003027267-A1.
ID ABS74409 standard; cDNA; 1234 BP.	PD 06-FEB-2003.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.	Query Match
PN US2002119130-A1.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PD 29-AUG-2002.	RESULT 1240
PA (GETH) GENENTECH INC.	ID ACEF13066 standard; cDNA; 1234 BP.
Query Match	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
Best Local Similarity 10.6%; Score 60.6; DB 6; Length 1234;	PN US2003036160-A1.
RESULT 1231	PD 20-FEB-2003.
ID ACA89493 standard; cDNA; 1234 BP.	Query Match
DE cDNA encoding human PRO polypeptide #119.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PN US2003036141-A1.	RESULT 1241
PD 20-FEB-2003.	ID ACD25169 standard; cDNA; 1234 BP.
Query Match	DE Human secreted/transmembrane protein (PRO) cDNA #119.
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	PN US2003044925-A1.
RESULT 1232	PD 06-MAR-2003.
ID ACA73503 standard; cDNA; 1234 BP.	Query Match
DE Human secreted/transmembrane protein (PRO) cDNA #119.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PN US2003036146-A1.	RESULT 1242
PD 20-FEB-2003.	ID ACF00218 standard; cDNA; 1234 BP.
PA (GETH) GENENTECH INC.	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
Query Match	PN US2003054474-A1.
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	PD 20-MAR-2003.
RESULT 1233	PA (GETH) GENENTECH INC.
ID ACA05818 standard; cDNA; 1234 BP.	Query Match
DE Human secreted/transmembrane protein (PRO) cDNA #119.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PD 06-FEB-2003.	RESULT 1243
PA (GETH) GENENTECH INC.	ID ACD25169 standard; cDNA; 1234 BP.
Query Match	DE Human secreted/transmembrane protein (PRO) cDNA #119.
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	PN US2003044925-A1.
RESULT 1244	PD 06-MAR-2003.
ID ACA05818 standard; cDNA; 1234 BP.	Query Match
DE Human secreted/transmembrane protein (PRO) cDNA #119.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PD 06-FEB-2003.	RESULT 1245
PA (GETH) GENENTECH INC.	ID ACF00218 standard; cDNA; 1234 BP.
Query Match	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	PN US2003054474-A1.
RESULT 1246	PD 20-MAR-2003.
ID ACA05818 standard; cDNA; 1234 BP.	PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein (PRO) cDNA #119.	Query Match
PD 06-FEB-2003.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
PA (GETH) GENENTECH INC.	RESULT 1247
Query Match	ID ACF00218 standard; cDNA; 1234 BP.
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
RESULT 1248	PN US2003054474-A1.
ID ACA05818 standard; cDNA; 1234 BP.	PD 20-MAR-2003.
DE Human secreted/transmembrane protein (PRO) cDNA #119.	PA (GETH) GENENTECH INC.
PD 06-FEB-2003.	Query Match
PA (GETH) GENENTECH INC.	Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
Query Match	RESULT 1249
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;	ID ACF00218 standard; cDNA; 1234 BP.
RESULT 1249	DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
ID ACA05818 standard; cDNA; 1234 BP.	PN US2003054474-A1.
DE Human secreted/transmembrane protein (PRO) cDNA #119.	PD 20-MAR

ID ACA60394 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1244
ID ACA72275 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1245
ID ACD04799 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1246
ID ACD18260 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1247
ID ACD08267 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1248
ID ACA88701 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1249
ID ACA70143 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1250
ID ACD12365 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1251
ID ACD15908 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1252
ID ACD24476 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1253
ID ACD17953 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1254
ID ACC88240 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1255
ID ACD21594 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1256
ID ACD18661 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1257
ID ACA58841 standard; cDNA; 1234 BP.
DE cDNA encoding human secreted polypeptide PRO3566.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1258
ID ABX98271 standard; cDNA; 1234 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 237.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1259
ID ACD14022 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1260
ID ACD09802 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1261
ID ACC88547 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1262
ID ACD21287 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1263
ID ABX75659 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3566.

PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1264
ID ACA64017 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1265
ID ABX97862 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1266
ID ACA97338 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1267
ID ACA57801 standard; cDNA; 1234 BP.
DE Human PRO3566 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1268
ID ACD14329 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1269
ID ACC91112 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1270
ID ACC88854 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1271
ID ACD07051 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1272
ID ACA67502 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1273
ID ACC81557 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1274
ID ACA91281 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1275
ID ACC89161 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1276
ID ACC86517 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1277
ID ACC89775 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1278
ID ACC92954 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1279
ID ACA72582 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1280
ID ACA89100 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1281
ID ACA69836 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1282
ID ACA96979 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1283
ID ACA90975 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032108-A1.

PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1284
ID ACA70757 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #119.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1285
ID ACA95267 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1286
ID ACC86210 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1287
ID ACD45180 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO3566 CDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1288
ID ACC9082 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1289
ID ACD12690 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #119.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1290
ID ACF19920 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1291
ID ABX76864 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1292
ID ACA73196 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1293
ID ACA68739 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003036136-A1.
PD 20-FEB-2003.

Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1294
ID ACA74583 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1295
ID ACA70450 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #119.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1296
ID ACD14636 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1297
ID ACA93728 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1298
ID ACA68308 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1299
ID ABX98773 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1300
ID ACA67302 standard; cDNA; 1234 BP.
DE CDNA encoding human secreted polypeptide PRO3566.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1301
ID ACC81250 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003021210-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1302
ID ACA95574 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1303
ID ACD04492 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 CDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;

Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1304			
ID	ACC87933 standard; cDNA; 1234 BP.		
DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.		
PN	US2003027281-A1.		
PD	06-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1305			
ID	ACFI2595 standard; cDNA; 1234 BP.		
DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.		
PN	US2003040085-A1.		
PD	27-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1306			
ID	ACH65275 standard; cDNA; 1234 BP.		
DE	Novel human secreted and transmembrane protein PRO3566 cDNA.		
PN	US2003027986-A1.		
PD	06-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1307			
ID	ACA96310 standard; cDNA; 1234 BP.		
DE	Human PRO polynucleotide #119.		
PN	US2003017540-A1.		
PD	23-JAN-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1308			
ID	ACA65084 standard; cDNA; 1234 BP.		
DE	Human PRO polynucleotide #119.		
PN	US2003032106-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1309			
ID	ACA73810 standard; cDNA; 1234 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #119.		
PN	US2003032129-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1310			
ID	ACA44222 standard; cDNA; 1234 BP.		
DE	Novel human secreted and transmembrane protein PRO3566 cDNA.		
PN	US2003032131-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1311			
ID	ACA96617 standard; cDNA; 1234 BP.		
DE	Human PRO polynucleotide #119.		
PN	US2003032103-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1312			
ID	ACDI0723 standard; cDNA; 1234 BP.		
DE	cDNA encoding human PRO polypeptide #119.		
PN	US2003032107-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1313			
ID	ACC9419 standard; cDNA; 1234 BP.		
DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.		
PN	US2003032133-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	
RESULT 1314			
ID	ACD9419 standard; cDNA; 1234 BP.		
DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.		
PN	US2003032133-A1.		
PD	13-FEB-2003.		
Query Match	10.6%;	Score 60.6;	DB 8; Length 1234;
Best Local Similarity	79.1%;	Pred. No. 0.18;	

RESULT 1314	ID	ACD02754 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;	Length 1234;
	DE	cDNA encoding human PRO polypeptide #119.				
	PN	US2003022301-A1.				
		30-JAN-2003.				
	Query Match					
	Best Local Similarity		10.6%;	Score 60.6;	DB 8;	Length 1234;
	RESULT 1315	ID	ACC87319 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237				
	PN	US2003036165-A1.				
		20-FEB-2003.				
	PA	(GETH) GENENTECH INC.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1316	ID	ACC85903 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237				
	PN	US2003027262-A1.				
		06-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1317	ID	ACA65391 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human PRO polynucleotide #119.				
	PN	US2003032110-A1.				
		13-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1318	ID	ACA94208 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				
	PN	US2003036142-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1319	ID	ACA97952 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human PRO polynucleotide #119.				
	PN	US2003036145-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1320	ID	ACA91454 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Novel human secreted and transmembrane protein PRO3566 cDNA.				
	PN	US2003036154-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1321	ID	ACA90668 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Novel human secreted and transmembrane protein PRO3566 cDNA.				
	PN	US2003036151-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1322	ID	ACD16215 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				
	PN	US2003044931-A1.				
		06-MAR-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1323	ID	ACD17376 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				
	PN	US2003036150-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1324	ID	ACA92033 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				
	PN	US2003036150-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1324	ID	ACA92033 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				
	PN	US2003036150-A1.				
		20-FEB-2003.				
	Query Match		10.6%;	Score 60.6;	DB 8;	Length 1234;
	Best Local Similarity		79.1%;	Pred. No. 0.18;		
	RESULT 1324	ID	ACA92033 standard; cDNA, 1234 BP.	10.6%;	Score 60.6;	DB 8;
	DE	Human secreted/transmembrane protein (PRO) cDNA #119.				

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1325
ID ACDD2329 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1326
ID ACA74890 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1327
ID ACA91761 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1328
ID ACA89320 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1329
ID ACA71405 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1330
ID ACC90805 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1331
ID ACA65815 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO protein #119.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1332
ID ACA88957 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1333
ID ACA94960 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1334
ID ACD16522 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1335
ID ACD15601 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1336
ID ACA98479 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #32.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1337
ID ABX16704 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein #119.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 8; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1338
ID ACA63404 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2003032042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1339
ID ACA97645 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1340
ID ACA99094 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1341
ID ACC91726 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1342
ID ACD1137 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1343
ID ACD14987 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1344
ID ACD11751 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1345
ID ACP95880 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1346
ID ACF16443 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1347
ID ACF02561 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1348
ID ACF02868 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1349
ID ACF21455 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1350
ID ACF10139 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1351
ID ACF78032 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1352
ID ACD46737 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1353
ID ACD49500 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1354
ID ACD49500 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1354
ID ACF28267 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1355
ID ACD88957 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1356
ID ACD84352 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1357
ID ACD99126 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1358
ID ADA77989 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1359
ID ACF48868 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1360
ID ACD09188 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US200306131-A1.
PD 20-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1361
ID ACF11981 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1362
ID ACF41215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1363
ID ACF15829 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1364
ID ACF16136 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1365
ID ACD31963 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1366
ID ACF18771 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1367
ID ACF09218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1368
ID ACF78339 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1369
ID ACF51938 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1370
ID ACF26425 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1371
ID ACF24218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1372
ID ACF63529 standard; cDNA; 1234 BP.

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1373
ID ACF50403 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1374
ID ACH07874 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1375
ID ACF13680 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1376
ID ACD41606 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1377
ID ACF32019 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1378
ID ACF23297 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1379
ID ACF39887 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1380
ID ACD45509 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1381
ID ACF53166 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003068721-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF27346 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068699-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF45184 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068707-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF29802 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073175-A1.
PA 17-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF29802 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073175-A1.
PA 17-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD9878 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068695-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD84659 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068703-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD98819 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068732-A1.
PA 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF77111 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082717-A1.
PA 01-MAY-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF76804 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104548-A1.
PA 05-JUN-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF49789 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104542-A1.
PA 05-JUN-2003.

Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF50096 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104543-A1.
PA 05-JUN-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD09495 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036127-A1.
PA 20-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD08574 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040061-A1.
PA 27-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACH03607 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.
PN US2003018172-A1.
PA 23-JAN-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF12288 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036130-A1.
PA 20-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACC94796 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054468-A1.
PA 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACD22515 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054470-A1.
PA 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACF15215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044917-A1.
PA 06-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACC97310 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044929-A1.
PA 06-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
ID ACC92340 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059880-A1.
PA 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1401
ID ACF13987 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1402
ID ACF14294 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1403
ID ACF09525 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1404
ID ACD45816 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1405
ID ACD47965 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1406
ID ACD67696 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1407
ID ACF25504 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1408
ID ACF29188 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1409
ID ACD6966 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1410
ID ACD84045 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1411
ID ACD88036 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1412
ID ACF30723 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1413
ID ACF32326 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1414
ID ACH11986 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1415
ID ACH12293 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1416
ID ADA19925 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1417
ID ACD40685 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1418
ID ADB17308 standard; cDNA; 1234 BP.
DE Human cDNA clone (SeqID 63) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

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RESULT 1419
ID ACF18157 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1420
ID ACF08604 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US200304978-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1421
ID ACF31405 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1422
ID ACF52245 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1423
ID ACD50114 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US200306873-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1424
ID ACF38817 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1425
ID ACF26732 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1426
ID ACF24832 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1427
ID ACF46412 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1428
ID ACF27960 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1429
ID ACD89264 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1430
ID ACF63836 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1431
ID ACF60476 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1432
ID ACHI2600 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1433
ID ACHI0023 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1434
ID ACD03878 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1435
ID ACD10416 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1436
ID ACD12058 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
RESULT 1437
ID ACF42443 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1438
ID ACF18464 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1439
ID ACF02254 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1440
ID ACF21762 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1441
ID ACF10446 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1442
ID ACF33898 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1443
ID ACF44860 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1444
ID ACD90492 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1445
ID ACD91105 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1446
ID ACF30416 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1447
ID ACD87115 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1448
ID ACF60169 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1449
ID ACF46719 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1450
ID ACF75576 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1451
ID ADA79781 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1452
ID ACF17236 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1453
ID ACF22990 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1454
ID ACF07990 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1455
ID ACF08297 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1456
ID ACF40601 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064448-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1457
ID ACF53780 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1458
ID ACD47044 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1459
ID ACF47947 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1460
ID ACF47333 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1461
ID ACF46105 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1462
ID ACD86194 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1463
ID ACF52552 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1464
ID ACF52859 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1465
ID ACF64852 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1466
ID ACF76497 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1467
ID ACF61397 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1468
ID ACF61704 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1469
ID ACD30735 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1470
ID ACD31656 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1471
ID ACD32577 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1472
ID ADA20097 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1473
ID ACD82121 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1474
ID ACF17543 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1475
ID ACF07376 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1476
ID ACF20534 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1477
ID ACF20841 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1478
ID ACF21148 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1479
ID ACD47658 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1480
ID ACF47640 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1481
ID ACF53473 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US200306879-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1482
ID ACD86808 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1483
ID ACH05056 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1484
ID ACF44553 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1485
ID ADA81508 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1486
ID ACD22208 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1487
ID ACD24555 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1488
ID ACD39758 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1489
ID ACD40065 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1490
ID ACF1373 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1491
ID ACF03175 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1492
ID ACF78646 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1493
ID ACF11367 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1494
ID ACF50710 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.

PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1495
ID ACF34205 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1496
ID ACD46430 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1497
ID ACD48272 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1498
ID ACF27653 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1499
ID ACF24525 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;
RESULT 1500
ID ACD85580 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 60.6; DB 9; Length 1234;
Best Local Similarity 79.1%; Pred. No. 0.18;